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OM protein - protein search, using SW model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-9
Perfect score: 664
Sequence: 1 ALELVTLGNIGKDGKQTLV.....AALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_23sep04:*
2: geneseqp1980s:*
3: geneseqp1980s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	664	100.0	132 5	ABG94320
2	664	100.0	132 5	ABG80632 Bacterioph
3	664	100.0	132 6	ABR56455 Bacterioph
4	664	100.0	132 6	ABU09693 Bacterioph
5	664	100.0	132 6	ABR44558 Bacterioph
6	664	100.0	132 7	ADD24133 Bacterioph
7	664	100.0	132 7	ADJ82059 Protein f
8	664	100.0	132 7	ADK17147 Virus-lik
9	664	100.0	132 8	ADJ36316 Bacterioph
10	664	100.0	132 8	ADJ67162 Phage Qbe
11	664	100.0	132 8	ADK52196 Bacterioph
12	661	99.5	132 5	ABG94319 PDB259 pr
13	661	99.5	132 5	ABG80631 Bacterioph
14	661	99.5	132 6	ABR56456 Bacterioph
15	661	99.5	132 6	ABU09692 Bacterioph
16	661	99.5	132 6	ABR44559 Bacterioph
17	661	99.5	132 7	ADD24134 Bacterioph
18	661	99.5	132 7	ADJ82060 Protein f
19	661	99.5	132 7	ADK17148 Virus-lik
20	661	99.5	132 8	ADJ36317 Bacterioph
21	661	99.5	132 8	ADJ67163 Phage Qbe
22	661	99.1	132 8	ADK52197 Bacterioph
23	658	99.1	132 5	ABG94316 PDB240 pr
24	658	99.1	132 5	ABG80628 Bacterioph
25	658	99.1	132 6	ABR56452 Bacterioph

26	658	99.1	132 6	ABU09689	ABU09689 Bacterioph
27	658	99.1	132 6	ABR44555	ABR44555 Bacterioph
28	658	99.1	132 7	ADD24130	ADD24130 Bacterioph
29	658	99.1	132 7	ADJ82056	ADJ82056 Protein f
30	658	99.1	132 7	ADK17144	ADK17144 Virus-lik
31	658	99.1	132 8	ADJ36313	ADJ36313 Bacterioph
32	658	99.1	132 8	ADJ67159	ADJ67159 Phage Qbe
33	658	99.1	132 8	ADK52193	ADK52193 Bacterioph
34	655	98.6	132 5	ABG94233	ABG94233 Bacterioph
35	655	98.6	132 5	ABG94318	ABG94318 PDB250 pr
36	655	98.6	132 5	ABG94317	ABG94317 PDB243 pr
37	655	98.6	132 5	ABG80629	ABG80629 Bacterioph
38	655	98.6	132 5	ABG80630	ABG80630 Bacterioph
39	655	98.6	132 5	ABG80545	ABG80545 Bacterioph
40	655	98.6	132 6	ABR56454	ABR56454 Bacterioph
41	655	98.6	132 6	ABR56459	ABR56459 Bacterioph
42	655	98.6	132 6	ABR56453	ABR56453 Bacterioph
43	655	98.6	132 6	ABU09686	ABU09686 Bacterioph
44	655	98.6	132 6	ABU09690	ABU09690 Bacterioph
45	655	98.6	132 6	ABU09691	ABU09691 Bacterioph

ALIGNMENTS

RESULT 1
ABG94320 standard; protein; 132 AA.

AC ABG94320;
DT 29-AUG-2003 (revised)
DT 10-DEC-2002 (first entry)
XX
XX PDB251 protein.
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
XX cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
XX vaccine; infectious disease.
XX unidentified bacteriophage.
XX WO200256905-A2.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-IB000166.
XX
XX 19-JAN-2001; 2001US-0262379P.
XX 04-MAY-2001; 2001US-0288549P.
XX 05-OCT-2001; 2001US-0326988P.
XX 07-NOV-2001; 2001US-0331045P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
XX Plossek C;
XX WPI, 2002-627351/67.
XX
XX Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX Claim 18; Page 426; 441pp; English.
XX
XX This invention relates to a novel ordered and repetitive antigen array
XX used in the production of vaccines for infectious diseases. The invention
XX also discloses a composition comprising a non-natural molecular scaffold
XX comprising a core particle selected from a core particle of a non-natural
XX origin and a core particle of natural origin and an organiser comprising
XX at least one first attachment site, where the organiser is connected to
XX the core particle by at least one covalent bond. Also disclosed is an
XX antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -Aug-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,3e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVPTNGVSLSGAGVPALEKRVTVSVSOPSRNRK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVPTNGVSLSGAGVPALEKRVTVSVSOPSRNRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 2
 ABG80632
 ID ABG80632 standard; protein; 132 AA.

XX ABG80632;

DT 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-259.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic aschma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angiotumproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enucleonase; cysteine-containing linker.

XX Bacteriophage Qbeta.
 OS Synthetic.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002MO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEBEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 PI Maurer P., Lechner F., Ortmann R., Luegend R., Staufenbiel M., Frey P;
 PI Renner WA, Bachmann M, Tiesot A, Sebbel P, Piossek C;
 XX WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

PS Example 18; Page 146; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an antigen or antigenic determinant with at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angiotumproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,3e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVPTNGVSLSGAGVPALEKRVTVSVSOPSRNRK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVPTNGVSLSGAGVPALEKRVTVSVSOPSRNRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 3
 ABR56455
 ID ABR56455 standard; protein; 132 AA.

Query Match	100.0%	Score 664	DB 6	Length 132
Best Local Similarity	100.0%	Pred. No. 2.3e-71		
Matches 132	Conservative 0	Mismatches 0	Indels 0	Gaps 0

1 AKLGFVTYLGNIKGKGRQTLVILNPGVNPFTNGVSLSGQCANPALKRRTVTSVSPDRNRK 60

Dd		1 AKLEVTLLGNIGKSGRQTLVINEPGRVNPTNGVASLSQGAVPALKEKRVTVSVSQPSRNK	60
Oy		61 NYKVQVKIQNFTACTANGSCDPSVTROKKYADVTFSFSTQYSTDEERAFVATELAAALASPL	120
Dd		61 NYKVQVKIQNFTACTANGSCDPSVTROKKYADVTFSFSTQYSTDEERAFVATELAAALASPL	120
Oy		121 LIDAIIDLNPAY	132
Dd		121 LIDAIIDLNPAY	132
RESULT 4			
ID	ABU09693	standard; protein, 132 AA.	
AC	ABU09693;		
DT	03-JUL-2003	(first entry)	
DE	Bacteriophage Qbeta mutant coat protein #5.		
KW	Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;		
KW	cardiant; nephroretropic; ophthalmological; immunostimulant; vaccine;		
KW	angiotensin peptide moiety carrier conjugate; angiotensin peptide;		
KW	renin-activated angiotensin system; hypertension; stroke; infarction;		
KW	congestive heart failure; kidney failure; retinal haemorrhage; mutant;		
XX			
OS	Bacteriophage Qbeta.		
PN	WO2003031466-A2.		
PD	17-APR-2003.		
PF	07-OCT-2002; 2002MO-BP011219.		
PR	05-OCT-2001; 2001US-0326989P.		
PR	07-NOV-2001; 2001US-0331045P.		
PR	18-JAN-2002; 2002US-00050902.		
PR	21-JAN-2002; 2002MO-IB000166.		
PR	19-JUL-2002; 2002US-0396637P.		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
PI	Bachmann M;		
DR	WPI, 2003-430264/40.		
PT	New angiotensin peptide moiety carrier conjugate comprising a carrier and		
PT	an angiotensin peptide moiety, useful for treating or preventing a		
PT	disorder associated with renin-activated angiotensin, e.g. hypertension		
PT	or infarction.		
Pt	Claim 20; Page 94; 97pp; English.		
XX			
XX	The invention describes an angiotensin peptide moiety carrier conjugate		
CC	comprising: (a) a carrier with at least one first attachment site; and		
CC	(b) at least one angiotensin peptide moiety with at least one second		
CC	attachment site. The angiotensin peptide conjugate and compositions		
CC	comprising them are useful for immunising an animal against an		
CC	angiotensin peptide, and for treating or preventing a physical disorder		
CC	associated with renin-activated angiotensin system such as hypertension,		
CC	stroke, infarction, congestive heart failure, kidney failure, and retinal		
CC	haemorrhage. The conjugate is also useful for inducing immune responses,		
CC	including producing antibodies. This is the amino acid sequence of a		
CC	mutant bacteriophage Qbeta coat protein used in the preparation of the		
CC	vaccine conjugates of the invention		
SQ	Sequence 132 AA;		
Query Match	100.0%; Score 664; DB 6; Length 132;		
Best Local Similarity	100.0%; Pred. No. 2.3e-71;		

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

QY 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBRAVFTETLALIASPL 120
 DB 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBRAVFTETLALIASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 5
 ABR44558 standard; protein; 132 AA.

XX ABR44558;
 XX AC
 XX DT 25-JUL-2003 (first entry)
 XX

DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:26.

XX
 XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytoskeletal; antiallergic; vitucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX WO2003024481-A2.

PN 27-MAR-2003.
 XX

PF 16-SEP-2002; 2002MO-IB004132.
 XX

PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.

XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR/) MAURER P.
 PA (TISS/) TISSOT A.
 PA (SCHW/) SCHWARZ K.
 PA (MEIJ/) MEIJERINK E.
 PA (LIPO/) LIPOMSKY G.
 PA (PUMP/) PUMPENS P.
 PA (CIEL/) CIELENS I.
 PA (RENH/) RENHOFA R.

XX
 XX Maurer P, Tisot A, Schwarz K, Meijerink E, Lipowsky G,
 PI Pumpens P, Cielems I, Renhofa R, Bachmann WF, Sornli T;
 DR WPI; 2003-354564/33.
 XX

PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX

PS Disclosure; Page 261-262; 322pp; English.
 XX

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytoskeletal, antiallergic, vitucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer),
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX

SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.3e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

QY 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBRAVFTETLALIASPL 120
 DB 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBRAVFTETLALIASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 6
 ADD24133
 ID ADD24133 standard; protein; 132 AA.
 XX

AC ADD24133;
 XX

DT 15-JAN-2004 (first entry)
 XX

DE Bacteriophage Qbeta coat protein mutant Qbeta-251.
 XX

XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; coat protein; mutant; mutein.

XX
 OS Synthetic.
 OS Bacteriophage Qbeta.
 XX WO2003059386-A2.
 PN 24-JUL-2003.
 XX

PD 17-JAN-2003; 2003MO-EP000460.
 XX

PF 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002MO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.

XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M, Maurer P, Pelllicoli E, Renner WA;
 PI WPI; 2003-598483/56.
 XX

DR A vaccine composition for preventing or treating prion diseases (e.g.
 XX

PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

XX Disclosure; SEQ ID NO 26; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (Prp) or its dimer, or a Prp-peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is the amino acid sequence of a mutant coat protein from bacteriophage Qbeta which may be used during the creation of the vaccine composition of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

QY 61 NTKVOYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFPVTELAALLASPL 120

DB 61 NTKVOYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFPVTELAALLASPL 120

QY 121 LIDAIQDQNPAY 132

DB 121 LIDAIQDQNPAY 132

RESULT 7

ADJ82059

ADJ82059 standard; proteain; 132 AA.

AC ADJ82059;

DT 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL; bone disease; encephalopathy; immune system stimulation.

XX Unidentified.

PN WO2003039225-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012449.

PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-441430/41.

XX New compositions comprising a core particle and at least one antigen or antigenic determinant, useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 26; 222pp; English.

XX The invention relates to a composition comprising a core particle having at least one first attachment site, and at least one antigen or antigenic determinant having at least one second attachment site. The antigen or antigenic determinant is a RANKL protein, RANKL fragment or RANKL peptide. The second attachment site is (non-) naturally occurring with the antigen or antigenic determinant, and is capable of association to the first attachment site. The antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful as a medicament, or for the manufacture of a medicament for treating bone diseases. The composition is especially useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies, and for stimulating mammalian immune system. This sequence represents a protein of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

QY 61 NTKVOYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFPVTELAALLASPL 120

DB 61 NTKVOYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFPVTELAALLASPL 120

QY 121 LIDAIQDQNPAY 132

DB 121 LIDAIQDQNPAY 132

RESULT 8

ADK17147

ADK17147 standard; peptide; 132 AA.

AC ADK17147;

DT 06-MAY-2004 (first entry)

DE Virus-like particle repetitive antigen array peptide #26.

KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle; interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;

KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

PN WO2003040164-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012455.

PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Jennings G, Sonderregger I;

XX WPI; 2003-441518/41.

XX Composition comprising an ordered and repetitive antigen or antigenic determinant array, useful as a medicament, or for manufacturing a medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's lymphoma.
XX
XX Disclosure; SEQ ID NO 26; 245pp; English.
XX
CC The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments, or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
SQ Sequence 132 AA:
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGKDGRTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNRK 60
Db 1 AKLEVTTLGNIGKDGRTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNRK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Db 61 NYKVQVKIOMPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 9
ADJ6316
ID ADJ6316 standard; protein; 132 AA.
XX
AC ADJ6316;
XX
DT 22-APR-2004 (first entry)
XX
DE Bacteriophage Qbeta coat protein virus-like particle mutant K2RK13R.
XX
KM anti-allergic; cytostatic; virucide; immunostimulant; vaccine;
KM immune response; virus-like particle; immunostimulatory; allergy; tumour;
KM chronic disease; chronic viral disease; bacteriophage Qbeta;
KM coat protein; VLP; adjuvant; mutant; mutein.
XX
OS Bacteriophage Qbeta.
XX
PN WO2004000351-A1.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-EP006541.
XX
PR 20-JUN-2002; 2002US-0389898P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Renner WA;
XX
DR WPI; 2004-108361/11.
XX
PT New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
XX Disclosure; SEQ ID NO 17; 252pp; English.
XX
CC The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
CC coat protein mutant, a virus like particle (VLP) that can be used in the
CC adjuvant of the invention.
XX
SQ Sequence 132 AA:
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGKDGRTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNRK 60
Db 1 AKLEVTTLGNIGKDGRTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNRK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Db 61 NYKVQVKIOMPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 10
ADJ67162
ID ADJ67162 standard; protein; 132 AA.
XX
AC ADJ67162;
XX
DT 06-MAY-2004 (first entry)
XX
DE Phage Qbeta coat protein mutant Qbeta 251 for antigen display array.
XX
KM anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
KM antigenic array.
XX
OS Bacteriophage Qbeta.
XX
PN WO2004009124-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-EP007849.
XX
PR 19-JUL-2002; 2002US-0396638P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Fulurija A;
XX
DR WPI; 2004-132866/13.
XX
PT New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.
XX
PS Disclosure; SEQ ID NO 20; 175pp; English.
XX
CC The invention relates to a new composition comprising: (i) a core
CC particle with at least one first attachment site; and (ii) at least one
CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the ghrelin or a
 CC ghrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC Qbeta coat protein mutant which can be used as part of the repetitive or
 CC antigenic array.

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.3e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0;

QY 1 AKLETTTLGNIGDGRQTLVLPNGVPTNGVSLSOAGAVPALERKVTYSVQPSRNRK 60

DB 1 AKLETTTLGNIGDGRQTLVLPNGVPTNGVSLSOAGAVPALERKVTYSVQPSRNRK 60

QY 61 NRVQYKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPL 120

DB 61 NRVQYKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPL 120

QY 121 LIDAIIDQLNPAY 132

DB 121 LIDAIIDQLNPAY 132

RESULT 11

ADK52196

ID ADK52196 standard; protein; 132 AA.

AC ADK52196;

DT 20-MAY-2004 (first entry)

XX Bacteriophage Qbeta coat protein mutant K16R A88K.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

XX core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX coat protein; CP; mutant; mutein.

XX Bacteriophage Qbeta.

XX Synthetic.

XX Key Location/Qualifiers

XX MISC-difference 16

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

XX MISC-difference 88

PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 PT such as Alzheimer's disease.

XX Example 1; SEQ ID NO 20; 184dp; English.

XX The invention describes a novel composition comprising a virus-like core

XX particle with at least one attachment site, and an antigenic amyloid beta

XX 1-6 peptide. The new composition comprises: a core particle with at least

XX one first attachment site; and at least one antigen or antigenic

XX determinant with at least one second attachment site, where the antigen

XX or antigenic determinant is a Amyloid beta 1-6 peptide, and where the

XX second attachment site comprises: an attachment site not naturally

XX occurring with the antigen or antigenic determinant; or an attachment

XX site naturally occurring with the antigen or antigenic determinant. The

XX second attachment site is capable of association to the first attachment

XX site and the beta 1-6 peptide and the core particle interact through the

XX association to form an ordered and repetitive antigen array. The

XX composition is useful for the manufacture of a medicament for treating

XX Alzheimer's disease and related diseases. This is the amino acid sequence

XX of an RNA bacteriophage Qbeta coat protein mutant that can be used in the

XX preparation of the compositions and vaccines of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.3e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0;

QY 1 AKLETTTLGNIGDGRQTLVLPNGVPTNGVSLSOAGAVPALERKVTYSVQPSRNRK 60

DB 1 AKLETTTLGNIGDGRQTLVLPNGVPTNGVSLSOAGAVPALERKVTYSVQPSRNRK 60

QY 61 NRVQYKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPL 120

DB 61 NRVQYKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPL 120

QY 121 LIDAIIDQLNPAY 132

DB 121 LIDAIIDQLNPAY 132

RESULT 12

ABG94319

ID ABG94319 standard; protein; 132 AA.

AC ABG94319;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

XX PQB259 protein.

XX Human; mouse; rat; antimicrobial; anti-allergic; immunomodulatory;

XX cytosolic; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

XX unidentified bacteriophage.

XX WO200256905-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002MO-IB000166.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326998P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Renner WA, Bachmann M, Tisbet A, Maurer P, Lechner F, Seibel P;

XX Plosek C;

XX Composition comprising a core particle with at least one attachment site,

XX WPI, 2002-627351/67.

XX Molecular antigen array used in the production of vaccines for infectious
PT diseases.

XX Claim 18; Page 146; 441p; English.

XX This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (A β 1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention. (Updated on 29
XX -AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 99.5%; Score 661; DB 5; Length 132;

Best Local Similarity 99.2%; Pred. No. 5.3e-71; Mismatches 0; Gaps 0;

Matches 131; Conservative 1; Indels 0; Indels 0;

QY 1 AKLETVLGNIGKDGROTLVLPNGVPTNGVSLGAGVPLERKVTYSVQSPNRK 60

Db 1 ARLETVLGNIGKDGROTLVLPNGVPTNGVSLGAGVPLERKVTYSVQSPNRK 60

QY 61 NYKQVXIQNPTRACTANGSCDPSTVRQKADVTFPSFTQYSTDEBRAFVETELALIASPL 120

Db 61 NYKQVXIQNPTRACTANGSCDPSTVRQKADVTFPSFTQYSTDEBRAFVETELALIASPL 120

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

QY 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

KW enterokinase; cysteine-containing linker.
XX Bacteriophage Qbeta.
OS Synthetic.
XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326988P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (NOVS) NOVARTIS PHARMA AG.

XX (MAUR) MAURER P.

XX (LECH) LECHNER F.

XX (ORTM) ORTMANN R.

XX (LUEB) LUEBEND R.

XX (STAU) STAUFENBIEL M.

XX (FREY) FREY P.

XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;

XX Renner WA, Bachmann M, Tissot A, Seibel P, Piossek C;

XX WPI, 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for infectious

XX diseases.

XX Example 18; Page 403; 418p; English.

XX The invention relates to a composition comprising: (a) a non-natural

XX molecular scaffold comprising: (i) a core particle selected from: (1) a

XX core particle of a non-natural origin; and (2) a core particle of natural

XX origin; and (ii) an organiser comprising at least one first attachment

XX site, where the organiser is connected to the core particle by at least

XX one covalent bond; (b) an antigen or antigenic determinant with at least

XX one second attachment site, where the antigen or antigenic determinant is

XX amyloid beta peptide (A β 1-42) or its fragment, and where the second

XX attachment site is selected from: (i) an attachment site not naturally

XX occurring with the antigen or antigenic determinant; and (ii) an

XX attachment site naturally occurring with the antigen or antigenic

XX determinant, where the second attachment site is capable of association

XX through at least one non-peptide bond to the first attachment site; and

XX where the antigen or antigenic determinant and the scaffold interact

XX through the association to form an ordered and repetitive antigen array.

XX Also included is a process for producing a non-naturally occurring

XX ordered and repetitive antigen array. The composition is used in

XX immunisation and as a vaccine for diseases such as influenza, graft

XX versus host disease, Igg-mediated allergic reactions, anaphylaxis, adult

XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,

XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,

XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia

XX gravis, immunoproliferative disease lymphadenopathy,

XX angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,

XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,

XX osteoporosis and infectious diseases. The antigens are modified to possess

XX a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-

XX or C-terminal linker peptide which serves as the attachment point to a

XX virus like particle or bacterial protein (the scaffold protein). The

XX present sequence is bacterial protein or peptide which is coupled to the

XX modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 99.5%; Score 661; DB 5; Length 132;

Best Local Similarity 99.2%; Pred. No. 5.3e-71;

Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
 DB 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132
 RESULT 14
 ABR56456 ID ABR56456 standard; protein; 132 AA.
 AC ABR56456;
 XX 28-JUL-2003 (first entry)
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:27.
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytoelastic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX WO2003024480-A2.
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-IB004252.
 PF 14-SEP-2001; 2001US-0318967P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann MF, Storni T, Lechner F;
 PI MPI; 2003-363095/34.
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX Disclosure; Page 183; 243pp; English.
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytoelastic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antineumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an

CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SO Sequence 132 AA:
 Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 5.3e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
 DB 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132
 RESULT 15
 ABU09692 ID ABU09692 standard; protein; 132 AA.
 AC ABU09692;
 XX 03-JUL-2003 (first entry)
 DE Bacteriophage Qbeta mutant coat protein #4.
 XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 XX Bacteriophage Qbeta.
 OS
 XX WO2003031466-A2.
 XX 17-APR-2003.
 PD 07-OCT-2002; 2002WO-EP011219.
 PF 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M;
 PI MPI; 2003-430264/40.
 XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX Claim 20; Page 94; 97pp; English.
 XX The invention describes an angiotensin peptide moiety carrier conjugate

CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage Opeta coat protein used in the preparation of the
CC vaccine conjugates of the invention

XX Sequence 132 AA;

SQ Query Match 99.5%; Score 661; DB 6; Length 132;

Best Local Similarity 99.2%; Pred. No. 5,3e-71; Mismatches 0; Gaps 0;

Matches 131; Conservative 1; Indels 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVINGVNPPTNGVSLSQAGAVPALERKRVTVSVSQPSRNRK 60
|:|||||
Db 1 ARLETVTLGNIGKDGROTLVINGVNPPTNGVSLSQAGAVPALERKRVTVSVSQPSRNRK 60

QY 61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDEBARFRTETLAAILASPL 120
|:|||||
Db 61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDEBARFRTETLAAILASPL 120

QY 121 LIDAIIDQLNPAY 132
|:|||||
Db 121 LIDAIIDQLNPAY 132

Search completed: January 4, 2005, 09:11:02
Job time : 40.6824 secs

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OM protein - protein search, using SW model

Run on: January 4, 2005, 09:05:21 : Search time 10.3622 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-9
Perfect score: 664
Sequence: 1 ALEFVTLGNICKDGRQTLV.....ALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
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4: /cgn2_6/prodata/1/aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	12.7	626	4 US-09-485-717-2	Sequence 2, Appl1
2	84.5	12.7	626	4 US-09-948-722-2	Sequence 2, Appl1
3	79.5	12.0	409	4 US-09-328-352-4249	Sequence 4249, Ap
4	74.5	11.2	916	4 US-09-252-991A-23637	Sequence 23637, A
5	71.5	10.8	383	3 US-09-045-186-2	Sequence 2, Appl1
6	71.5	10.8	384	1 US-08-232-144-4	Sequence 4, Appl1
7	71.5	10.8	384	2 US-08-555-268A-15	Sequence 15, Appl
8	71.5	10.8	384	3 US-09-200-673-15	Sequence 15, Appl
9	71.5	10.8	384	4 US-10-013-846-4	Sequence 4, Appl1
10	71.5	10.8	384	4 US-09-708-392-9	Sequence 9, Appl1
11	71.5	10.8	384	5 PCT-US93-05039-3	Sequence 3, Appl1
12	71.5	10.8	411	3 US-08-817-869-3	Sequence 3, Appl1
13	71.5	10.8	411	5 PCT-US95-14377-3	Sequence 3, Appl1
14	71	10.7	233	3 US-08-725-459B-45	Sequence 45, Appl
15	71	10.7	341	3 US-08-725-459B-44	Sequence 44, Appl
16	71	10.7	434	3 US-08-725-459B-42	Sequence 42, Appl
17	70.5	10.6	502	4 US-09-270-767-44620	Sequence 44620, A
18	69.5	10.5	129	1 US-08-090-148-1	Sequence 1, Appl1
19	69	10.4	766	4 US-09-538-092-216	Sequence 216, App
20	69	10.4	1073	4 US-09-206-942-49	Sequence 49, Appl
21	69	10.4	1079	4 US-09-206-942-47	Sequence 47, Appl
22	68.5	10.3	569	4 US-09-248-796A-20249	Sequence 20249, A
23	68.5	10.3	733	4 US-09-248-796A-16565	Sequence 16565, A
24	68.5	10.3	1036	2 US-08-720-484A-5	Sequence 5, Appl1
25	68.5	10.3	1036	3 US-08-953-823A-5	Sequence 5, Appl1
26	68.5	10.3	1036	4 US-09-398-239-5	Sequence 5, Appl1
27	68.5	10.3	1036	4 US-09-560-876A-5	Sequence 5, Appl1

28	68.5	10.3	1065	4 US-09-560-876A-6	Sequence 6, Appl1
29	68	10.2	316	4 US-09-270-767-43925	Sequence 43925, A
30	68	10.2	316	4 US-09-270-767-59331	Sequence 59331, A
31	68	10.2	345	3 US-08-856-253-7	Sequence 7, Appl1
32	68	10.2	933	3 US-08-293-728-2	Sequence 2, Appl1
33	68	10.2	933	3 US-09-421-868-2	Sequence 2, Appl1
34	68	10.2	936	4 US-08-956-171E-5249	Sequence 5249, Ap
35	68	10.2	936	4 US-08-781-986A-5249	Sequence 5249, Ap
36	67.5	10.2	1328	4 US-08-781-891-76	Sequence 76, Appl
37	67.5	10.2	1328	4 US-09-618-166-76	Sequence 76, Appl
38	67	10.1	632	4 US-09-976-594-41	Sequence 41, Appl
39	67	10.1	3892	4 US-09-328-352-5503	Sequence 5503, Ap
40	66.5	10.0	279	3 US-08-397-411-13	Sequence 13, Appl
41	66.5	10.0	424	3 US-09-173-581-7	Sequence 7, Appl1
42	66.5	10.0	424	3 US-09-420-915-7	Sequence 7, Appl1
43	66.5	10.0	428	3 US-09-134-001C-2885	Sequence 2885, Ap
44	66	9.9	1281	2 US-08-843-530B-6	Sequence 6, Appl1
45	66	9.9	1281	4 US-09-636-728-5	Sequence 5, Appl1

ALIGNMENTS

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RESULT 1
US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan
; APPLICANT: Hees, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862PUS
; CURRENT APPLICATION NUMBER: US/09/485, 717
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2
Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best local Similarity 22.7%; Pred. No. 0.16;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGRLVLT-----NKGVPFNGVSLSGQA-----VPALEKRV 48
DB 138 KDNENYIVVEKKKKSINQNNADIQVNAISLTPALVANSSELVENQDPVLPVKRDSL 197
QY 49 TVSVSPSRNRKRYKQVQKIONFTACANGSCDPVTR-----OKYADTFSGTOYSTD 102
DB 198 TLSIDLPKMTGNTDKKIVK--NATKSNVNNVNTLVERNKEKYAOATPNVS---AKIDYD 252
QY 103 EERAPVTEILAA 114
DB 253 DEMAYSESQSLA 264
RESULT 2
US-09-948-722-2
; Sequence 2, Application US/09948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan H. E.
; APPLICANT: Hees, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine
```


FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match.
Best Local Similarity 12.7%; Score 84.5; DB 4; Length 626;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGKQTLVL-----NPRGVNPTNGVSLQAGA-----VPALKRY 48
DB 138 KDGKHYIVKRRKKSINQNNADIQVNAISLTYFGLVKANSELVENQDVLVKKDSL 197
QY 49 TVSVSOPSRNKNKYQVKIONPACTANGSCDSVTR-----QKADYTFSTQYSTD 102
DB 198 TUSIDLEGMTQMDKIYVK--NATKSVNNAVNLTVERMEKVAQAVPNVS---AKIDYD 252
QY 103 EERAFVETELAA 114
DB 253 DEMAYSESQLIA 264

RESULT 3
US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match
Best Local Similarity 12.0%; Score 79.5; DB 4; Length 409;
Matches 35; Conservative 19; Mismatches 53; Indels 25; Gaps 6;

QY 7 TLGNIGKDGKQTLVLN---PR-----GVNPTNGVSLQAGAVPALERKRYTV-SVSPS 56
DB 109 SLINFTKDVAGGGRILNANNVRNMLISPAVNVDTGTP-----IAKPNQSLITRIDLLAG 163
QY 57 RNRKNKYQVKIONPACTANGSCDSVTRQKYADYTFSTQYSTDERRAFVETELAA 116
DB 164 RTGSN---ALAYAREGFTNNALVENVETAKPYSEITF-----EAVESVKTIAHMLK 213
QY 117 ASPLLDALDOL 128
DB 214 ASKQIUDDLPOL 225

RESULT 4
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match
Best Local Similarity 11.2%; Score 74.5; DB 4; Length 916;
Matches 28; Conservative 16; Mismatches 53; Indels 21; Gaps 4;

QY 9 GNIGKDG-----RQTLVNPGRVNPNGVSLQAGAVPALERKRYTVS-----QP 55
DB 789 GLTGGEGALRLALMAIVVARRRIDPQGLAALPVGGALPALQADFAFGSLDQRYQA 848
QY 56 SRNRKNKYQVKIONPACTANGSCDSVTRQKYADYTFSTQYSTDERRAFVET 110
DB 849 EERGAETRAQESAHREPCRSIEANADCPLSADAGK-----PWITFSQATRMALRT 901

RESULT 5
US-09-045-186-2
Sequence 2, Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn
TITLE OF INVENTION: RHBSUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-09-200-673-15

Query Match 10.8%; Score 71.5; DB 3; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNTN-----GVA---SLSDAGAVPALEKRVTVSVSPSRNRKRYQVK 67
DB 138 RQHLINPRGWRPNRRHAYVGIWVLA VASSLPFLIYO--VMTDEPQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKYADVTFSTFOYSTDEERAFVRELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRSLTYTLTLVL 218

RESULT 9

US-10-013-846-4
Sequence 4; Application US/10013846
Patent No. 6566367
GENERAL INFORMATION:
APPLICANT: Baktavatchalam, Rajagopal
APPLICANT: Blum, Charles A
APPLICANT: Brielmann, Harry L
APPLICANT: Darrow, James W
APPLICANT: De Lombaert, Stephane
APPLICANT: Hutchinson, Alan
APPLICANT: Ryan, Jennifer
APPLICANT: Zheng, Xiaozhang
APPLICANT: Elliott, Richard L
APPLICANT: Hammond, Marlys
TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
TITLE OF INVENTION: 3H-spiro[isobenzofuran-1,4'-piperidines
FILE REFERENCE: N00.2001
CURRENT APPLICATION NUMBER: US/10/013.846
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,990
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 384
TYPE: PRT
ORGANISM: homosapiens
US-10-013-846-4

Query Match 10.8%; Score 71.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNTN-----GVA---SLSDAGAVPALEKRVTVSVSPSRNRKRYQVK 67
DB 138 RQHLINPRGWRPNRRHAYVGIWVLA VASSLPFLIYO--VMTDEPQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKYADVTFSTFOYSTDEERAFVRELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRSLTYTLTLVL 218

RESULT 10
US-09-708-392-9
Sequence 9; Application US/09708392
Patent No. 6734186

GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Maw, G

TITLE OF INVENTION: Pharmaceutical
FILE REFERENCE: PCI0343AAM
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 9926437.6
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 0004021.2
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 0016563.9
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: GB 0017141.3
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 60/221,014
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/221,093
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-09-708-392-9

Query Match 10.8%; Score 71.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNTN-----GVA---SLSDAGAVPALEKRVTVSVSPSRNRKRYQVK 67
DB 138 RQHLINPRGWRPNRRHAYVGIWVLA VASSLPFLIYO--VMTDEPQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKYADVTFSTFOYSTDEERAFVRELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRSLTYTLTLVL 218

RESULT 11

PCT-US93-05039-3
Sequence 3; Application PC/TUS9305039

GENERAL INFORMATION:
APPLICANT: Claes R. Wahlestedt
TITLE OF INVENTION: Human Neuropeptide Y/peptide YY
TITLE OF INVENTION: Receptor of the Y1-Type and
TITLE OF INVENTION: Antisense Oligonucleotides
TITLE OF INVENTION: Thereto Which Inhibit Vasoconstriction
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/05039
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-05039-3

Query Match 10.8%; Score 71.5; DB 5; Length 384;
Best Local Similarity 25.9%; Pred. No.3.2; Indels 35; Gaps 4;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

Qy 16 RQTLVLPNGVNPNTN-----GVA---SLSQAGVPALEKRVTVSVSPSRNRKRYKQVK 67
Db 138 RHQLINPGRMNRNNHAYGVIAVWLA VASSLPFLIYQ--VMTDEPQN----- 186
Qy 68 IQNPACTANGSCDPSVTRQKADVTFSTQYSTDEERAFVTELAAL 115
Db 187 -----VTLDAYKDKYVCDFQPSDSHRLSYTLLVL 218

RESULT 12
US-08-817-869-3
; Sequence 3, Application US/08817869
; Patent No. 6001970
; GENERAL INFORMATION:
; APPLICANT: STRADER, CATHERINE D.
; APPLICANT: CASCIERI, MARGARET A.
; APPLICANT: MACNEIL, DOUGLAS J.
; TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM H. NICHOLSON
; STREET: 126 EAST LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,017
; FILING DATE: 07-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NICHOLSON, WILLIAM H.
; REGISTRATION NUMBER: 25,147
; REFERENCE/DOCKET NUMBER: 19339Y PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-1348
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-817-869-3

Query Match 10.8%; Score 71.5; DB 3; Length 411;

Best Local Similarity 25.9%; Pred. No.3.6;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;
Qy 16 RQTLVLPNGVNPNTN-----GVA---SLSQAGVPALEKRVTVSVSPSRNRKRYKQVK 67
Db 141 RHQLINPGRMNRNNHAYGVIAVWLA VASSLPFLIYQ--VMTDEPQN----- 189
Qy 68 IQNPACTANGSCDPSVTRQKADVTFSTQYSTDEERAFVTELAAL 115
Db 190 -----VTLDAYKDKYVCDFQPSDSHRLSYTLLVL 221

RESULT 13
PCT-US95-14377-3
; Sequence 3, Application PC/TUS9514377
; GENERAL INFORMATION:
; APPLICANT: STRADER, CATHERINE D.
; APPLICANT: CASCIERI, MARGARET A.
; APPLICANT: MACNEIL, DOUGLAS J.
; TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: 126 EAST LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,017
; FILING DATE: 07-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19339Y PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3462
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-14377-3

Query Match 10.8%; Score 71.5; DB 5; Length 411;
Best Local Similarity 25.9%; Pred. No.3.6; Indels 35; Gaps 4;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

Qy 16 RQTLVLPNGVNPNTN-----GVA---SLSQAGVPALEKRVTVSVSPSRNRKRYKQVK 67
Db 141 RHQLINPGRMNRNNHAYGVIAVWLA VASSLPFLIYQ--VMTDEPQN----- 189
Qy 68 IQNPACTANGSCDPSVTRQKADVTFSTQYSTDEERAFVTELAAL 115
Db 190 -----VTLDAYKDKYVCDFQPSDSHRLSYTLLVL 221

RESULT 14
US-08-725-459B-45
; Sequence 45, Application US/08725459B
; Patent No. 6084068

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; GENERAL INFORMATION:
; APPLICANT: CONAWAY, RONALD C.
; APPLICANT: CONAWAY, JOAN W.
; TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SIDLEY & AUSTIN
; STREET: 717 N. HARWOOD, SUITE 3400
; CITY: DALLAS
; STATE: TX
; COUNTRY: US
; ZIP: 75201-6507
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,459B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HANSEN, EUGENIA S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: 11146/07501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-981-3300
; TELEFAX: 214-981-3400
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..233
; OTHER INFORMATION: /note="amino acids 202-434 of C.
; OTHER INFORMATION: elegans"
; US-08-725-459B-45

Query Match 10.7%; Score 71; DB 3; Length 233;
Best Local Similarity 33.7%; Pred. No. 1.7;
Matches 32; Conservative 11; Mismatches 38; Indels 14; Gaps 5;

QY 2 KLETVTLGNIGK-----DGRQTLVLPNGVNPFTNGVASLSQAGV--PALEKRVTVSVS 53
DB 116 KLEMLT-SRIGKNSAOSQGRQTMVIDMAHTR---VRSKSPFTYKDSQVKMSATPSPAL 170
QY 54 QPSRNRKNYKVQYKIQNPACTANGSCDPSVTRQK 88
DB 171 QLSQARKNVKIEGKAQLRT-ITPRGGGVSTSRSR 204

RESULT 15
US-08-725-459B-44
; Sequence 44, Application US/08725459B
; Patent No. 6084068
; GENERAL INFORMATION:
; APPLICANT: CONAWAY, RONALD C.
; APPLICANT: CONAWAY, JOAN W.
; TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SIDLEY & AUSTIN
; STREET: 717 N. HARWOOD, SUITE 3400
; CITY: DALLAS
; STATE: TX
; COUNTRY: US
; ZIP: 75201-6507
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,459B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HANSEN, EUGENIA S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: 11146/07501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-981-3300
; TELEFAX: 214-981-3400
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..341
; OTHER INFORMATION: /note="amino acids 94-434 of C.
; OTHER INFORMATION: elegans"
; US-08-725-459B-44

Query Match 10.7%; Score 71; DB 3; Length 341;
Best Local Similarity 33.7%; Pred. No. 3.1;
Matches 32; Conservative 11; Mismatches 38; Indels 14; Gaps 5;

QY 2 KLETVTLGNIGK-----DGRQTLVLPNGVNPFTNGVASLSQAGV--PALEKRVTVSVS 53
DB 224 KLEMLT-SRIGKNSAOSQGRQTMVIDMAHTR---VRSKSPFTYKDSQVKMSATPSPAL 278
QY 54 QPSRNRKNYKVQYKIQNPACTANGSCDPSVTRQK 88
DB 279 QLSQARKNVKIEGKAQLRT-ITPRGGGVSTSRSR 312
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Search completed: January 4, 2005, 09:35:45
Job time: 11.3622 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664
Sequence: 1 AKLEVTTLGNIGKDGQTLV.....AALLSPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA.*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	14	US-10-243-739-26 Sequence 26, Appl
2	664	100.0	132	14	US-10-244-065-26 Sequence 26, Appl
3	664	100.0	132	14	US-10-289-454-26 Sequence 26, Appl
4	664	100.0	132	14	US-10-050-902-259 Sequence 259, App
5	664	100.0	132	14	US-10-050-898-259 Sequence 259, App
6	664	100.0	132	14	US-10-346-190-26 Sequence 26, Appl
7	664	100.0	132	15	US-10-465-811-17 Sequence 17, Appl
8	664	100.0	132	15	US-10-289-456-26 Sequence 26, Appl
9	664	100.0	132	15	US-10-622-064-9 Sequence 9, Appl
10	664	100.0	132	15	US-10-622-124-20 Sequence 20, Appl
11	664	100.0	132	16	US-10-622-087-20 Sequence 20, Appl
12	661	99.5	132	14	US-10-243-739-27 Sequence 27, Appl
13	661	99.5	132	14	US-10-244-065-27 Sequence 27, Appl

14	661	99.5	132	14	US-10-289-454-27	Sequence 27, Appl
15	661	99.5	132	14	US-10-050-902-258	Sequence 258, App
16	661	99.5	132	14	US-10-050-898-258	Sequence 258, App
17	661	99.5	132	14	US-10-346-190-27	Sequence 27, Appl
18	661	99.5	132	15	US-10-465-811-18	Sequence 18, Appl
19	661	99.5	132	15	US-10-289-456-27	Sequence 27, Appl
20	661	99.5	132	15	US-10-622-064-10	Sequence 10, Appl
21	661	99.5	132	15	US-10-622-124-21	Sequence 21, Appl
22	661	99.5	132	16	US-10-622-087-21	Sequence 21, Appl
23	661	99.5	132	14	US-10-243-739-23	Sequence 23, Appl
24	661	99.5	132	14	US-10-244-065-23	Sequence 23, Appl
25	661	99.5	132	14	US-10-289-454-23	Sequence 23, Appl
26	661	99.5	132	14	US-10-050-902-255	Sequence 255, App
27	661	99.5	132	14	US-10-050-898-255	Sequence 255, App
28	661	99.5	132	14	US-10-346-190-23	Sequence 23, Appl
29	661	99.5	132	15	US-10-465-811-14	Sequence 14, Appl
30	661	99.5	132	15	US-10-289-456-23	Sequence 23, Appl
31	661	99.5	132	15	US-10-622-064-6	Sequence 6, Appl
32	661	99.5	132	15	US-10-622-124-17	Sequence 17, Appl
33	661	99.5	132	16	US-10-622-087-17	Sequence 17, Appl
34	661	99.5	132	14	US-10-243-739-10	Sequence 10, Appl
35	661	99.5	132	14	US-10-243-739-24	Sequence 24, Appl
36	661	99.5	132	14	US-10-243-739-25	Sequence 25, Appl
37	661	99.5	132	14	US-10-244-065-10	Sequence 10, Appl
38	661	99.5	132	14	US-10-244-065-24	Sequence 24, Appl
39	661	99.5	132	14	US-10-244-065-25	Sequence 25, Appl
40	661	99.5	132	14	US-10-289-454-10	Sequence 10, Appl
41	661	99.5	132	14	US-10-289-454-24	Sequence 24, Appl
42	661	99.5	132	14	US-10-289-454-25	Sequence 25, Appl
43	661	99.5	132	14	US-10-050-902-259	Sequence 259, App
44	661	99.5	132	14	US-10-050-902-256	Sequence 256, App
45	661	99.5	132	14	US-10-050-902-257	Sequence 257, App

ALIGNMENTS

RESULT 1
US-10-243-739-26
; Sequence 26, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storn, Tazio
; APPLICANT: lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243, 739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318, 967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPNGVNASLSQAQAVPALERKRVVVSQPSRRNK 60
DB 1 AKLEVTTLGNIGKDGQTLVLPNGVNPNGVNASLSQAQAVPALERKRVVVSQPSRRNK 60
QY 61 NYVQVKINPACTANGSCDPSVTRKQYADYTFSTQSTDEERAFVTELAALASPL 120
DB 61 NYVQVKINPACTANGSCDPSVTRKQYADYTFSTQSTDEERAFVTELAALASPL 120
QY 121 LIDAIDQNPAY 132

Db 121 LIDAIQDLPAY 132

RESULT 2

US-10-244-065-26
; Sequence 26, Application US/10244065
; Publication No. US2003009668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornil, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRNRK 60
DB 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 3

US-10-289-454-26
; Sequence 26, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta-251
US-10-289-454-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRNRK 60
DB 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 4

US-10-050-902-259
; Sequence 259, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 259
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 251
US-10-050-902-259

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRNRK 60
DB 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 5
US-10-050-898-259
; Sequence 259, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piosek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; TYPE: PRT
; LENGTH: 132
; ORGANISM: Qb 251
US-10-050-898-259

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGQRTVLNPRGVNPTNGVSLSOAGAVPALERKVTYVSQPSNRK 60
DB 1 AKLETVTLGNIGDGQRTVLNPRGVNPTNGVSLSOAGAVPALERKVTYVSQPSNRK 60

QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADYVFSFTQYSTDERAFVRLTAALLASPL 120
DB 61 NYKVQVKIQNPCTANGSCDPSVTRQKADYVFSFTQYSTDERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 6
US-10-346-190-26
; Sequence 26, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 251
US-10-346-190-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGQRTVLNPRGVNPTNGVSLSOAGAVPALERKVTYVSQPSNRK 60
DB 1 AKLETVTLGNIGDGQRTVLNPRGVNPTNGVSLSOAGAVPALERKVTYVSQPSNRK 60

QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADYVFSFTQYSTDERAFVRLTAALLASPL 120
DB 61 NYKVQVKIQNPCTANGSCDPSVTRQKADYVFSFTQYSTDERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 7
US-10-465-811-17
; Sequence 17, Application US/10465811
; Publication No. US2004000538A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
US-10-465-811-17

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGQRTVLNPRGVNPTNGVSLSOAGAVPALERKVTYVSQPSNRK 60
DB 1 AKLETVTLGNIGDGQRTVLNPRGVNPTNGVSLSOAGAVPALERKVTYVSQPSNRK 60

QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADYVFSFTQYSTDERAFVRLTAALLASPL 120
DB 61 NYKVQVKIQNPCTANGSCDPSVTRQKADYVFSFTQYSTDERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 8
US-10-289-456-26
; Sequence 26, Application US/10289456

Publication No. US2004003211A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.2
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 251 mutant
US-10-289-456-26

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
DB 1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
61 NYKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
DB 61 NYKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
QY 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 9
US-10-622-064-9
Sequence 9, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick P
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,575
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
US-10-622-064-9

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60

DB 1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
QY 61 NYKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
DB 61 NYKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
QY 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 10
US-10-622-124-20
Sequence 20, Application US/10622124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurja, Alma
TITLE OF INVENTION: Ghrelin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,638
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 20
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
US-10-622-124-20

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
DB 1 AKLEVTTLGNIGKDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
61 NYKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
DB 61 NYKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
QY 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 11
US-10-622-087-20
Sequence 20, Application US/10622087
Publication No. US20040141964A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tisect, Alain
APPLICANT: Ortman, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Staendlel, Matthias
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin version 3.2
SEQ ID NO 20

LENGTH: 132.
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
 US-10-622-087-20

Query Match 100.0%; Score 664; DB 16; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.6e-66;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVNIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETELAAALSPL 120
 DB 61 NYKVQVNIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETELAAALSPL 120

QY 121 LIDALDQNLNPAY 132
 DB 121 LIDALDQNLNPAY 132

RESULT 12
 US-10-243-739-27
 Sequence 27, Application US/10243739
 Publication No. US20030091593A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin F.
 APPLICANT: Storn, Tazio
 APPLICANT: Lechner, Franziska
 TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
 TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
 FILE REFERENCE: 1700.0210001
 CURRENT APPLICATION NUMBER: US/10/243.739
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/318,967
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Bacteriophage Q-beta
 US-10-243-739-27

Query Match 99.5%; Score 661; DB 14; Length 132;
 Best Local Similarity 99.2%; Pred. No. 3.5e-66;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVNIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETELAAALSPL 120
 DB 61 NYKVQVNIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETELAAALSPL 120
 QY 121 LIDALDQNLNPAY 132
 DB 121 LIDALDQNLNPAY 132

RESULT 13
 US-10-244-065-27
 Sequence 27, Application US/10244065
 Publication No. US20030099668A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin F.
 APPLICANT: Storn, Tazio
 APPLICANT: Maurer, Patrick
 APPLICANT: Tissot, Alain

APPLICANT: Schwarz, Katrin
 APPLICANT: Meijerink, Edwin
 APPLICANT: Lipowsky, Gerard
 APPLICANT: Pumpens, Paul
 APPLICANT: Cielens, Indulis
 APPLICANT: Renhota, Regina
 TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
 TITLE OF INVENTION: Method of Preparation and Use
 FILE REFERENCE: 1700.0230001
 CURRENT APPLICATION NUMBER: US/10/244.065
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/374,145
 PRIOR FILING DATE: 2002-04-22
 PRIOR APPLICATION NUMBER: 60/318,994
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Bacteriophage Q-beta
 US-10-244-065-27

Query Match 99.5%; Score 661; DB 14; Length 132;
 Best Local Similarity 99.2%; Pred. No. 3.5e-66;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVNIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETELAAALSPL 120
 DB 61 NYKVQVNIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETELAAALSPL 120
 QY 121 LIDALDQNLNPAY 132
 DB 121 LIDALDQNLNPAY 132

RESULT 14
 US-10-289-454-27
 Sequence 27, Application US/10289454
 Publication No. US20030157479A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin
 APPLICANT: Demings, Gary
 APPLICANT: Sonderegger, Ivo
 TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
 FILE REFERENCE: 1700.0360001
 CURRENT APPLICATION NUMBER: US/10/289.454
 CURRENT FILING DATE: 2003-02-10
 PRIOR APPLICATION NUMBER: US 60/396,636
 PRIOR FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: PCT/IB02/00166
 PRIOR FILING DATE: 2002-01-21
 PRIOR APPLICATION NUMBER: US 10/050,902
 PRIOR FILING DATE: 2002-01-18
 PRIOR APPLICATION NUMBER: US 60/331,045
 PRIOR FILING DATE: 2001-11-07
 NUMBER OF SEQ ID NOS: 386
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 27
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Bacteriophage Q-beta-259
 US-10-289-454-27

Query Match 99.5%; Score 661; DB 14; Length 132;
 Best Local Similarity 99.2%; Pred. No. 3.5e-66;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

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Db      1 ARLETVTLGNIGDGRQTLVLPNGVNPPTNGVASLSQAGAVPALKKRTVSVSQPSNRK 60
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Qy      61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSTQYSTDERAFVRTLAALLASPL 120
      |||||
Db      61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSTQYSTDERAFVRTLAALLASPL 120
      |||||
Qy      121 LIDAIQOLNPAY 132
      |||||
Db      121 LIDAIQOLNPAY 132
      |||||
```

RESULT 15

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US-10-050-902-258
; Sequence 258, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 258
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
; US-10-050-902-258
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Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AKLETVTLGNIGDGRQTLVLPNGVNPPTNGVASLSQAGAVPALKKRTVSVSQPSNRK 60
      |:|||||
Db      1 ARLETVTLGNIGDGRQTLVLPNGVNPPTNGVASLSQAGAVPALKKRTVSVSQPSNRK 60
      |||||
Qy      61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSTQYSTDERAFVRTLAALLASPL 120
      |||||
Db      61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSTQYSTDERAFVRTLAALLASPL 120
      |||||
Qy      121 LIDAIQOLNPAY 132
      |||||
Db      121 LIDAIQOLNPAY 132
      |||||
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Search completed: January 4, 2005, 09:41:23
Job time : 33.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 : Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664
Sequence: 1 AKLEVTTLGNIGDKGRQTLV.....ALLASPLLDALDQLNPAV 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	98.6	132	1	VCBPQB coat protein - pha
2	531.5	80.0	331	2	S01964 readthrough protei
3	116	17.5	131	1	VCBPPI coat protein - pha
4	89.5	13.5	530	2	S22340 seeligertolysin -
5	85.5	12.9	540	2	T00646 hypothetical prote
6	84.5	12.7	529	2	S24231 listeriolysin prec
7	84.5	12.7	529	2	A43505 listeriolysin O pr
8	84.5	12.7	529	2	AC1100 listeriolysin O pr
9	80.5	12.1	528	2	S22341 ivanolysin precurs
10	80.5	12.1	1502	1	RGBYH1 CYC1/CYP3 transcr
11	79	11.9	282	2	A10186 probable iron-side
12	79	11.9	432	2	T31660 hypothetical prote
13	78	11.7	830	2	S57537 MMT1 protein - yea
14	76.5	11.5	136	2	C98221 conserved hypochet
15	76.5	11.5	136	2	AE3065 conserved hypochet
16	76.5	11.5	1052	2	G64221 hypothetical 114k
17	76.5	11.5	1861	2	T13845 microtubule-assoc
18	75.5	11.4	1097	2	AD2522 hypothetical prote
19	75	11.3	130	1	A46324 coat protein - pha
20	75	11.3	130	1	VCBPQA coat protein - pha
21	74.5	11.2	130	1	VCBPER coat protein - pha
22	74.5	11.2	161	4	I55480 hypothetical natr
23	74	11.1	340	2	S18650 homeotic protein H
24	74	11.1	340	2	A42008 homeotic protein H
25	73.5	11.1	191	2	H90078 hypothetical prote
26	73.5	11.1	520	1	ACMSD1 nicotinic acetylch
27	73.5	11.1	601	2	A55921 serine/threonine k
28	73.5	11.1	719	2	T39271 conserved hypochet
29	73	11.0	430	2	G88884 protein K09B11.10

30	72.5	10.9	129	1	VCBPF2 coat protein - pha
31	72.5	10.9	129	1	VCBPR7 coat protein - pha
32	72.5	10.9	129	1	VCBPR7 coat protein - pha
33	72.5	10.9	289	2	C70400 ferredoxin oxidore
34	72	10.8	376	2	C84316 hypothetical prote
35	71.5	10.8	384	2	A45490 neuropeptide y/pep
36	71.5	10.8	458	2	T49114 hypothetical prote
37	71.5	10.8	654	2	S69673 SAC7 protein - yea
38	71	10.7	248	2	A86786 conserved hypochet
39	71	10.7	366	2	F70618 probable putaa pro
40	71	10.7	399	1	A43685 polymerase-associ
41	71	10.7	434	2	S72430 transcription elon
42	71	10.7	434	2	D88305 protein R03D7.4 [l
43	71	10.7	463	2	S00676 translaation elonga
44	71	10.7	1461	2	E90696 hypothetical prote
45	71	10.7	1461	2	A85547 hypothetical prote

ALIGNMENTS

RESULT 1

VCBPQB coat protein - phage Q-beta

C:Species: phage Q-beta

C:Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004

C:Accession: A92240; A92221; A92088; A04224

R:Biscarmis, C.; Sactery, P.A.; Billeter, M.A.

J. Biol. Chem. 253, 8390-8399, 1978

A:Title: Determination of the first half of the coat protein cistron of bacteriophage Qb

A:Reference number: A92240; PMID:79048469; PMID:361741

A:Accession: A92240

A:Molecule type: mRNA

A:Residues: 1-80 <ESG>

A:Cross-references: UNIPROT:P03615

J. Stoll, E.; Wilson, K.J.; Reiser, J.; Weisemann, C.

J. Biol. Chem. 252, 990-993, 1977

A:Title: Revised amino acid sequence of Obeta coat protein between positions 1 and 60.

A:Reference number: A92221; PMID:77118576; PMID:838709

A:Accession: A92221

A:Molecule type: protein

A:Residues: 1-60 <STO>

R:Malta, T.; Konigsberg, W.

J. Biol. Chem. 246, 5003-5024, 1971

A:Title: The amino acid sequence of the Obeta coat protein.

A:Reference number: A92088; PMID:7128580; PMID:5570434

A:Accession: A92088

A:Molecule type: protein

A:Residues: 1-21, 'D', '23-55, 57-132 <MAI>

C:Superfamily: phage GA coat protein

Query Match 98.6%; Score 655; DB 1; Length 132;

Best Local Similarity 98.5%; Pred. No. 1e-56;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	AKLEVTTLGNIGDKGRQTLVNPRTNGVSLSOAGVPALEKRVTVSOPSNRK 60	
DB	1	AKLEVTTLGNIGDKGRQTLVNPRTNGVSLSOAGVPALEKRVTVSOPSNRK 60	
QY	61	NYKVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFAVTELAALLASPL 120	
DB	61	NYKVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFAVTELAALLASPL 120	
QY	121	LIDALDQLNPAV 132	
DB	121	LIDALDQLNPAV 132	

RESULT 2

S01964 readthrough protein - phage SP

C:Species: phage SP

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

A/Residues: 1-529 <RAS>
A/Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PIDN:CAA42639.1; PID:g44112
A/Experimental source: strain 12067, serotype 4b
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C/Genetics:
A/Gene: 116A
C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domains: signal sequence #status predicted <SIG>
F/26-529/Product: listeriolysin #status predicted <MAT>
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KGGRTLVL-----NPRGVNPTNGVASLSQAGA-----VPALRKRV 48
DB 93 KGGNEIYVEKKKKKSNQNNADIQVNVALLSLTPGALVKANSELVENQPDVLPVKRDSL 152
QY 49 TVSVSQPSRRKKRYKVQVQKIQNPACTANGSCDPSVTR-----QKYADVTSFTQYSTD 102
DB 153 TTSIDLPGMTNQDNKLVK--NATKSNVNNVAVTLVERNMEKKAQAYPNVS---AKIDYD 207
QY 103 EERAFVRTIELAA 114
DB 208 DEMAYSESQILIA 219
RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C/Species: Listeria monocytogenes
C/Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C/Accession: A43505; S05306; A47606; S12400; A61079
R/Mengaud, J.; Vicens, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanzey
Infect. Immun. 56, 766-772, 1988
A/Title: Expression in *Escherichia coli* and sequence analysis of the listeriolysin O det
A/Reference number: A43505; MUID:88153053; PMID:3126142
A/Accession: A43505
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <MEN>
A/Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PIDN:AAA03018.1; PID:g149653
A/Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R/Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A/Title: Nucleotide sequence of the listeriolysin gene from a *Listeria monocytogenes* ser
A/Reference number: S05306; MUID:89366684; PMID:2505236
A/Accession: S05306
A/Molecule type: DNA
A/Residues: 1-529 <DOM>
A/Cross-references: EMBL:X15127; NID:g44106; PIDN:CAA33223.1; PID:g44107
A/Experimental source: strain EGD
A/Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R/Mengaud, J.; Chenevert, J.; Geoffroy, C.; Gallard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3227, 1987
A/Title: Identification of the structural gene encoding the SH-activated hemolysin of *Li*
A/Reference number: A47606; MUID:88057627; PMID:2824384
A/Accession: A47606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 413-480 <ME2>
A/Cross-references: GB:M29171
R/Michel, E.; Reich, K.A.; Favler, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A/Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A/Reference number: S12400; MUID:91211627; PMID:1965218
A/Accession: S12400
A/Molecule type: DNA
A/Residues: 483-493 <MIC>
A/Experimental source: strain LO28, serotype 1/2c
C/Genetics:
A/Gene: hlyA; 116A

C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domains: signal sequence #status predicted <SIG>
F/26-529/Product: listeriolysin O #status predicted <MAT>
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KGGRTLVL-----NPRGVNPTNGVASLSQAGA-----VPALRKRV 48
DB 93 KGGNEIYVEKKKKKSNQNNADIQVNVALLSLTPGALVKANSELVENQPDVLPVKRDSL 152
QY 49 TVSVSQPSRRKKRYKVQVQKIQNPACTANGSCDPSVTR-----QKYADVTSFTQYSTD 102
DB 153 TTSIDLPGMTNQDNKLVK--NATKSNVNNVAVTLVERNMEKKAQAYPNVS---AKIDYD 207
QY 103 EERAFVRTIELAA 114
DB 208 DEMAYSESQILIA 219
RESULT 8
AC1100
Listeriolysin O precursor [imported] - *Listeria monocytogenes* (strain EGD-e)
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC1100
R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseigneur, O.; Entian, K.D.; Feihl, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Krefz, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tjerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of *Listeria* species
A/Reference number: AB1077; MUID:2157279; PMID:11679669
A/Accession: AC1100
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <GLA>
A/Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:g16409567; GSPDB:(
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: hly
C/Superfamily: dipeptide transport protein
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KGGRTLVL-----NPRGVNPTNGVASLSQAGA-----VPALRKRV 48
DB 93 KGGNEIYVEKKKKKSNQNNADIQVNVALLSLTPGALVKANSELVENQPDVLPVKRDSL 152
QY 49 TVSVSQPSRRKKRYKVQVQKIQNPACTANGSCDPSVTR-----QKYADVTSFTQYSTD 102
DB 153 TTSIDLPGMTNQDNKLVK--NATKSNVNNVAVTLVERNMEKKAQAYPNVS---AKIDYD 207
QY 103 EERAFVRTIELAA 114
DB 208 DEMAYSESQILIA 219
RESULT 9
S22341
Ivanovysin precursor - *Listeria ivanovii*
C/Species: *Listeria ivanovii*
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S22341; S36683
R/Haas, A.; Dumbeky, M.; Krefz, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A/Title: Listeriolysin genes: complete sequence of ilo from *Listeria ivanovii* and of leo
A/Reference number: S22340; MUID:92182018; PMID:1543752

A:Accession: S22341
 A:Molecule type: DNA
 A:Residues: 1-528 <HAS>
 A:Cross-references: UNIPROT:P31831; EMBL:X60461
 A>Note: the authors translated the codon ACA for residue 331 as Val
 R:Kieft, U.
 Submitted to the EMBL Data Library, July 1991
 A:Reference number: S36683
 A:Accession: S36683
 A:Molecule type: DNA
 A:Residues: 1-319, 'T', 321-528 <KRB>
 A:Cross-references: EMBL:X60461
 C:Genetics:
 A:Gene: 110
 C:Superfamily: dipeptide transport protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-528/Product: tyrosylsine #status predicted <MAT>

Query Match 12.1%; Score 80.5; DB 2; Length 528;
 Best Local Similarity 22.0%; Pred. No. 5.5;
 Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGROTLVLP-----NRGVNPTNGVSLSGAG-----VPALEKRY 48
 Db 92 KEGNQYIVVKKKKKSNQNNADIQVNSLSLTPGALVKANSELVENQPDVLPVKRDSV 151
 QY 49 TVGVSDPSRRKRYKVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
 Db 152 TLSDIDLP--GMVNHNDNIIVQNNATKSNINGVTLVDKRNKKSEEPNIS---AKIDVD 206
 QY 103 EERAFVTELA 114
 Db 207 QEMAYSESQVLA 218

RESULT 10

RGBYH1
 CYC1/CPY3 transcription activator - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein L9672.1; protein YLR256w; regulatory protein CYP1; regulatory
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Sep-1991 #sequence revision 23-Feb-1996 #text_change 12-Nov-1999
 C:Accession: S59400; A31312; G15447; S05804; S15446
 R:Johnson, D.
 Submitted to the EMBL Data Library, February 1995
 A:Description: The sequence of S. cerevisiae cosmid 9672.
 A:Reference number: S59386
 A:Accession: S59400
 A:Molecule type: DNA
 A:Residues: 1-1502 <JOH>
 A:Cross-references: EMBL:U20865; NID:G662330; PID:AA67387.1; PID:G662331; GSPDB:GN0001
 A:Experimental source: strain S288C (AB972)
 R:Feifer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
 Cell 56, 291-301, 1989
 A:Title: Functional dissection and sequence of yeast HAP1 activator.
 A:Reference number: A31312; MUID:89106221; PMID:2643482
 A:Accession: A31312

A:Molecule type: DNA
 A:Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'W', 509-586, 'K', 588-882, 'N', 884-95
 A:Cross-references: EMBL:J03152; NID:G171645; PID:AA34662.1; PID:G171646
 R:Creusot, F.; Verdier, J.; Gaisne, M.; Slonimski, P.P.
 J. Mol. Biol. 204, 263-276, 1988
 A:Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
 A:Reference number: S15447; MUID:89125585; PMID:2851658
 A:Accession: S15447
 A:Molecule type: DNA
 A:Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPFIW' <CREI>
 A:Cross-references: EMBL:X13793
 A>Note: the sequence is from mutant CYP1-18
 C:Genetics:
 A:Gene: SGD:HAP1, CYP1, MIPS:YLR256w
 A:Cross-references: SGD:S0004246; MIPS:YLR256w
 A:Map position: 12R
 C:Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology

C:Keywords: DNA binding; heme binding; transcription regulation; zinc finger
 F:1-148/Domain: DNA binding #status predicted <DNA>
 F:159-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:64-84/Region: zinc finger CCCC motif
 F:177-189/Region: glutamine-rich
 F:245-445/Domain: heme binding #status predicted <HEM>
 F:299-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats
 F:1308-1481/Domain: activation element #status predicted <ACT>
 F:1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
 Best Local Similarity 20.6%; Pred. No. 18;
 Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;

QY 23 PRGVN--PTNGVSL-----SQGAVPALEKRYTVSVS 53
 Db 1278 PRGISKPSNGSLSSVPLSSFSMNQNGTIPVPSLNTISQMALSLSDITTNQIN 1337
 QY 54 QPSRRN-KRYKVQKIQNP-----TACTANGSCP 82
 Db 1338 LPDPSRDEAFDINSIKQMTPTSAFNANNTTIPSTLNGNMNMGACTAATDTSANGSALS 1397
 QY 83 SVTRQKXADV-TFSFQYSTD--EERAFVTELAALASP-LLIDALQAN 129
 Db 1398 TLTSFGSGLASNSATQYKPDLEDFLMQNSNENGLMINSLEVEVGGYN 1447

RESULT 11

A10186
 Probable iron-siderophore transport system, ATP-binding component YPO1533 [imported] - Ye
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A10186
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 demo-tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB00001; MUID:21470413; PMID:11586360
 A:Accession: A10186
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <KUR>
 A:Cross-references: UNIPROT:Q8ZF20; GB:AL590842; PID:CA090356.1; PID:G15979576; GSPDB:GT
 C:Genetics:
 A:Gene: YPO1533
 C:Superfamily: inner membrane protein malX; ATP-binding cassette homology

Query Match 11.9%; Score 79; DB 2; Length 282;
 Best Local Similarity 22.0%; Pred. No. 3.7;
 Matches 27; Conservative 37; Mismatches 45; Indels 14; Gaps 5;

QY 13 KDGROTLVNPQVNPNTNGVSLSGAGVPALEKRYTVSPSRKRYKVQKIQNP 72
 Db 49 KNGAFSVITGPNCGCKSTLLRLRS---LIPQNSIRLDQ--QIQYKAKVPAKQIS 102
 QY 73 ACTANGSCPVS-----RQKYADVTFSTGYSTDEERAFVTELAALASP-LLIDAL 126
 Db 103 LLSQGSISSETITVPLVSRGYAQS-F-FHQWSTEDER-IVKALISAVNLSISVQGRVS 160
 QY 127 QAN 129
 Db 161 ELS 163

RESULT 12

T31660
 Hypothetical protein COS41.6 - sea squirt (Cliona intestinalis)
 C:Species: Cliona intestinalis
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T31660
 R:Bird, A.P.; Clark, V.; Jones, S.J.; Leisgeb, S.; Dobson, R.; Tweedle, S.
 submitted to the EMBL Data Library, December 1996

A:Accession: Z21049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-332 <BIR>
A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289966; PIDN:CAB0605
C:Genetics:
A:Introns: 180/2; 212/1; 229/3

Query Match 11.9%; Score 79; DB 2; Length 432;
Best Local Similarity 28.3%; Pred. No. 6.1;
Matches 32; Conservative 16; Mismatches 47; Indels 18; Gaps 6;

Oy 4 ETVTLGNIGKQGRQTLVINGRCVNPFGVNSLSDAGAVPALEKRYTVSVSPSRKRYK 63
Db 242 DTSEGEVTKXGPNLENP--TPSNARELQESVSEVLETVVNSAID-EODSSAYR 297
64 VQVNIQNPAC-TANGSC-----DPSVTRQKAD-----VTFSPFOYSTDE 103
Db 298 KE-NPQNPACPNRNGNCVSTNSKTPFDSKLEIVNDSDDNTTDEDIOTIDPNE 349

RESULT 13
S57537
MKTI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N2302; protein YNL085w
C:Species: Saccharomyces cerevisiae
C:Date: 10-Oct-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
A:Accession: S57537; S50279; S63024; S63017; S65096
R:Solier-Mita, A.; Salt, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57537
A:Accession: S57537
A:Molecule type: DNA
A:Residues: 1-830 <SOE>
A:Cross-references: UNIPROT:P40850; EMBL:X89016; NID:G887621; PID:G887626
R:Vermet, M.; Widner, W.R.; Dimman, J.D.; Wickner, R.B.
Yeast 10, 1477-1479, 1994
A:Title: Sequence of MKTI, needed for propagation of M(2) satellite dsRNA of the L-A virus
A:Reference number: S50279; MUID:95176705; PMID:7532890
A:Accession: S50279
A:Molecule type: DNA
A:Residues: 1-29, 'G', 31-808, 'TMKTCIANYH' <VER>
A:Cross-references: EMBL:U09129; NID:G520475; PIDN:AAC94940.1; PID:G520476
R:Solier-Mita, A.; Salt, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63018
A:Accession: S63024
A:Molecule type: DNA
A:Residues: 1-830 <SOE>
A:Cross-references: EMBL:Z71361; NID:G1301982; PID:G1301983; MIPS:YNL085w
R:Poehlmann, R.; Philippaen, P.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S63017
A:Molecule type: DNA
A:Residues: 569-830 <POE>
A:Cross-references: EMBL:Z71361; MIPS:YNL085w
A:Experimental source: strain S288C
R:Solier-Mita, A.; Salt, J.E.; Ballesta, J.P.G.; Remacha, M.
Yeast 12, 485-491, 1996
A:Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
A:Reference number: S65092; MUID:96310628; PMID:8740422
A:Accession: S65096
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-830 <SOF>
A:Cross-references: EMBL:X89016; NID:G887621; PIDN:CAA61425.1; PID:G887626
C:Genetics:
A:Gene: SGD:MKTI
A:Cross-references: SGD:S0005029; MIPS:YNL085w
A:Map position: 14L

C:Superfamily: Saccharomyces cerevisiae MKT1 protein
 C:Keywords: transmembrane protein
 F:615-631/Domain: transmembrane #status predicted <tm>

 Query Match 11.7%; Score 78; DB 2; Length 830;
 Best Local Similarity 24.8%; Pred. No. 16;
 Matches 25; Conservative 21; Mismatches 49; Indels 6; Gaps 3;

 QY 5 TTTLTGKIGKGRQTLVLPNGVPTNGVASLSQAGVPALEKRVVSVSQPSRNNKYAV 64
 Db 301 STTLQN--DSKENIQNYQRGISALRYPVLKDTGKVLFGVEIVASBESEKNNKDGK- 356
 QY 65 QVKIQNPPACTANGSCDPSVTRKQYADVTFSFTQYSTDEER 105
 Db 357 KSNLSPS--SASSASAPATTVTYKNASEKLTYESKSTKVR 395

 RESULT 14
 C98221
 hypothetical protein AGR_L1428 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: C98221
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappae, C.; Markelz, B.;
 Science 294, 2223-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C98221
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KUR>
 A:Cross-references: UNIPROT:Q8U8F3; GB:AE007870; PIDN:AAK89293.1; PID:g15159127; GSPDB:G
 C:Genetics:
 A:Gene: AGR_L1428
 A:Map position: linear chromosome

 Query Match 11.5%; Score 76.5; DB 2; Length 136;
 Best Local Similarity 24.6%; Pred. No. 2.8;
 Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

 Db 11 IGKGRQTLVLPNGVPTNGVASLSQAGV-----PALEKRVTVSVSQPSRRR 59
 QY 3 ISKGRQTESADPHKIEWVTGTISTLVAAMGMAIYDIRSPBARPEIATVGTGEGQT 62
 Db 60 KNYKQVQKIQNPACTA-----NGSCDPSVTRKQYADVTFSF-TQYSTDEERAFVTE 111
 QY 63 GQYVKFPIHNLSTTAQVAVVVRGDLQNGASPENADVTFDVVASSESKNGTLFFRSD 120

 RESULT 15
 AE3065
 conserved hypothetical protein Atu4139 [imported] - Agrobacterium tumefaciens (strain C5f
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AE3065
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 R:Wood, D.W.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,
 J.; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE3065
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KUR>
 A:Cross-references: UNIPROT:Q8U8F3; GB:AE008669; PIDN:AAL44939.1; PID:g17742593; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4139
 A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;
 Best Local Similarity 24.6%; Pred. No. 2.8;
 Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;
 QY 11 IGDGRQTLVLPFGVNPPTNGVASLSQAGV-----PALEKRVTVSVSOPSRRR 59
 Db 3 ISKDGKQTESADPHWIEWVTGTISTLLVAMPFWIAYDIYRYSPEEARFEIATGVGGQT 62
 QY 60 KNYKQVQKIQNPTACTA-----NGSCDPSYTRQKADVTFSF--TQYSTDERAFV RTE 111
 Db 63 GQYRVKFAIHNLMTTAAQVNVRGDLEQNGASPENADVTFPDYVASEKONGTLFFRSD 120

Search completed: January 4, 2005, 09:17:31
 Job time : 9.03224 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664
Sequence: 1 AKLETVLGNIGKRGQTLV.....AALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_spot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	98.6	132	1	COAT_BPOBE
2	655	98.6	132	2	AAM33126
3	655	98.6	329	2	O8LTF1
4	655	98.6	329	2	AAL1663
5	566	85.2	133	2	O9TOR9
6	566	85.2	329	2	O64307
7	546	82.2	133	2	O9TOR9
8	546	82.2	329	2	O64303
9	531.5	80.0	132	1	COAT_BPSP
10	531.5	80.0	331	1	VAL_BPSP
11	499.5	75.2	132	2	O9TOR8
12	499.5	75.2	330	2	O64310
13	116	17.5	131	1	COAT_BPFR
14	96.5	14.5	473	2	O8VDC2
15	89.5	13.5	530	1	TACY_LISSE
16	89.5	13.5	530	2	AAP97361
17	85.5	12.9	540	2	O48683
18	84.5	12.7	529	1	TACY_LISMF
19	84.5	12.7	529	1	TACY_LISMO
20	84.5	12.7	529	2	O9L5B9
21	84.5	12.7	529	2	O6E942
22	84.5	12.7	529	2	O6E9A2
23	84.5	12.7	529	2	O6E9G2
24	84.5	12.7	529	2	O6E9Q2
25	84.5	12.7	529	2	O6E9T2
26	84.5	12.7	529	2	O6E9A28
27	84.5	12.7	529	2	O6E9A6
28	84.5	12.7	529	2	O6E9A7
29	84.5	12.7	529	2	O6E9A0
30	84.5	12.7	529	2	O6E9A4
31	84.5	12.7	529	2	AAT03000

32	82	12.3	1624	2	O9V3K8	O9V3K8 drosophila
33	82	12.3	1637	2	O95R08	O95R08 drosophila
34	81	12.2	336	2	O8TRF3	O8TRF3 methanocarc
35	80.5	12.1	528	1	TACY_LISIV	P31631 listeria iv
36	80.5	12.1	528	2	O6R6D9	O6R6D9 listeria iv
37	80.5	12.1	528	2	AAP97343	AAP97343 listeria
38	80.5	12.1	1502	1	CYPI_YEAST	P12351 baccharomyc
39	79.5	12.0	608	2	O84H79	O84H79 rhodococcus
40	79	11.9	282	2	O8ZPZ0	O8ZPZ0 yersinia pe
41	79	11.9	282	2	AAS61663	AAS61663 yersinia
42	79	11.9	325	2	O73R79	O73R79 treponema d
43	79	11.9	325	2	AAS10709	AAS10709 treponema
44	79	11.9	432	2	P91584	P91584 ciona inter
45	79	11.9	512	2	O6HGA7	O6HGA7 bacillus th

ALIGNMENTS

RESULT 1
COAT_BPOBE STANDARD; PRT; 132 AA.
ID COAT_BPOBE
AC P03615;
DT 21-UTL-1986 (Rel. 01, Created)
DT 21-UTL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviriviruses.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielesni I., Drellina D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RT assembled in Escherichia coli.",
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmis C., Sastre P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
RT bacteriophage Q-beta as an application of a mapping procedure for RNA
RT fragments.",
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Scoll B., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
RT and 60.",
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiz T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.",
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Valgard K., Lilljas L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.",
RL Structure 4:543-554(1996).
CC 1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
or send an email to license@isb-sib.ch.

DR EMBL, M99039; AAA16662.1; -.
DR EMBL, V00643; CAA23992.1; -.
DR PIR, A92240; VCBPOB.
DR PDB, 1QBE; X-ray; A/B/C=1-132.
DR InterPro, IPR002703; Levi coat.
DR Pfam, PF01819; Levi coat; 1.
KM 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
FT INIT MET 0 0
FT CONFLICT 22 22 N -> D (in Ref. 4).
FT CONFLICT 56 56 Missing (in Ref. 4).
FT STRAND 6 9
FT TURN 13 14
FT STRAND 18 27
FT STRAND 28 31
FT STRAND 32 36
FT HELIX 42 44
FT STRAND 47 53
FT STRAND 56 56
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 74
FT STRAND 83 96
FT TURN 98 99
FT HELIX 102 117
FT HELIX 119 126
FT TURN 127 127
SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.6%; Score 655; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 1.7e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
DB 1 AKLEVTTLGNIGDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVTELAALIASPL 120
DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVTELAALIASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 2
AA33126 PRELIMINARY; PRT; 133 AA.
ID AA33126
AC AA33126;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses; Alloviridae subgroup III.
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
DR EMBL, AY099114; AA33126.1; -.
KW Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.6%; Score 655; DB 2; Length 133;
Best Local Similarity 98.5%; Pred. No. 1.7e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
DB 2 AKLEVTTLGNIGDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVTELAALIASPL 121
QY 121 LIDAIDQLNPAY 132
DB 122 LIDAIDQLNPAY 133

RESULT 3
O8LTEL1 PRELIMINARY; PRT; 329 AA.
ID O8LTEL1
AC O8LTEL1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses.
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Dreilina D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-assembled in Escherichia coli."
RL Gene 137:133-137(1993).
DR EMBL, AY099114; AA33127.1; -.
DR EMBL, M99039; AAA16663.1; -.
DR HSSP; P03615; 1QBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Levi_coat_1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.6%; Score 655; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 4.8e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
DB 2 AKLEVTTLGNIGDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVTELAALIASPL 121

QY 121 LIDAIDQLNPAY 132
DB 122 LIDAIDQLNPAY 133

RESULT 4
AAA16663 PRELIMINARY; PRT; 329 AA.
ID AAA16663
AC AAA16663;
DT 02-MAR-2004 (TReMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE A1 protein
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
ON NCBI_TaxID=12009;
OX (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clemons I., Dreilina D., Dislers A., Baumanis V.,
Ose V., Pumpens P.,
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
assembled in Escherichia coli."
RT Gene 137:133-137(1993).
RL EMBL, M99039; AAA16663.1; --
DR SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;
SQ

Query Match 98.6%; Score 655; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 4, 8e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 60
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DB 2 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 61
QY 61 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 120
DB 62 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 121
QY 121 LIDAIQDLPNPAY 132
DB 122 LIDAIQDLPNPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.

ID Q9TOR9;
AC Q9TOR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
ON NCBI_TaxID=75723;
OX (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta."
RT J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RT J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14699.1; --
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;
SQ

Query Match 85.2%; Score 566; DB 2; Length 133;
Best Local Similarity 83.3%; Pred. No. 7, 1e-47;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 60
DB 2 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 61
QY 61 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 120
DB 62 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 121
QY 121 LIDAIQDLPNPAY 132
DB 122 LIDAIQDLPNPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.

ID O64307;
AC O64307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DB 2 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 61
QY 61 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 120
DB 62 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 121
QY 121 LIDAIQDLPNPAY 132
DB 122 LIDAIQDLPNPAY 133

RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta."
RT J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RT J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14700.1; --
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;
SQ

Query Match 85.2%; Score 566; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 2e-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 60
DB 2 AKLEVTTLNIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSQPSRNRK 61
QY 61 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 120
DB 62 NRVQVQKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFVRETELAAALASPL 121
QY 121 LIDAIQDLPNPAY 132
DB 122 LIDAIQDLPNPAY 133

ID	Q9T0S0	PRELIMINARY;	PRT;	133 AA.
AC	Q9T0S0			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Coat protein.			
OS	Bacteriophage M11.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;			
CC	Allolevivirus.			
OX	NCBI_TaxID=74336;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95239761; PubMed=7723040;			
RA	Beekwilder M.J., Nieuwenhuizen R., van Duin J.;			
RT	"Secondary structure model for the last two domains of single-stranded			
RL	RNA phage Q beta.";			
RL	J. Mol. Biol. 247:903-917(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96190948; PubMed=8609616;			
RA	Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;			
RT	"Secondary structure model for the first three domains of Q beta RNA.			
RL	Control of A-protein synthesis.";			
RL	J. Mol. Biol. 256:8-19(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;			
RL	Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF052431; AAC06250.1; ..			
DR	HSSP; P03615; IOBE.			
DR	GO; GO:0019028; C:Viral capsid; IEA.			
DR	GO; GO:0005198; F:Structural molecule activity; IEA.			
DR	InterPro; IPR002703; Lev1 coat.			
DR	Pfam; PF01819; Lev1_coat; 1.			
KW	Cost protein.			
SC	SEQUENCE 133 AA; 14198 MW; 098722E3C6C3A255 CRC64;			
Query Match	82.2%; Score 546; DB 2; Length 133;			
Best Local Similarity	80.3%; Pred. No. 6,1e-45;			
Matches 106; Conservative 12; Mismatches 14; Indels 0; Gaps 0;				
QY	1 AKLETVLIGNIGKGRQTVLVNPRGVNPTNGVSLISQAGVPALEKRYTVSVSOPSRNRK 60			
DB	2 AKLQAITLSGIGKGDVTLDLNPRGVNPTNGVVALSEAGAVPALEKRYTVISVSOPSRNRK 61			
QY	61 NYKQVQKIONFTACANGSCDPSTYRQKADVTSTFOYSTDEBRAPVETLALLLSPL 120			
DB	62 NYKQVQKIONFTCTSHAGSCDPSTYRQKADVTSTFOYSTDEBRAPVETLALLLSPL 121			
QY	121 LIDAIDQLNPAY 132			
DB	122 LVNAIDNLNPAY 133			
RESULT 8				
ID	064303	PRELIMINARY;	PRT;	329 AA.
AC	064303			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	A1-protein.			
OS	Bacteriophage M11.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;			
CC	Allolevivirus.			
OX	NCBI_TaxID=74336;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95239761; PubMed=7723040;			

```

RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;  

RA "Secondary structure model for the last two domains of single-stranded  

RT RNA phage Q beta."  

RL J. Mol. Biol. 247:903-917(1995).  

RN [2]  

RN SEQUENCE FROM N.A.  

RP MEDLINE=96190948; PubMed=8609616;  

RX Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;  

RT "Secondary structure model for the first three domains of Q beta RNA.  

RT Control of A-protein synthesis."  

RL J. Mol. Biol. 256:8-19(1996).  

RN [3]  

RN SEQUENCE FROM N.A.  

RP Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;  

RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  

DR EMBL, AF0522431; AAC06251.1; -.  

DR HSSP, P03615; IOBE.  

DR GO, GO:0019028; C:viral capsid; IEA.  

DR GO, GO:0005198; F:structural molecule activity; IEA.  

DR InterPro, IPR002703; Levi.coat.  

DR InterPro, IPR000504; RNA_rec_mot.  

DR Pfam, PF01819; Levi.coat.1.  

DR PROSITE, PS00030; RM_RNP_1; UNKNOWN.1.  

SO SEQUENCE 329 AA; 35693 MW; 3E33CD821EE625F4 CRC64;  

  

Query Match 82.2%; Score 546; DB 2; Length 329;  

Best Local Similarity 80.3%; Pred. No. 1,8e-44;  

Matches 106; Conservative %12; Mismatches 14; Indels 0; Gaps 0;  

  

QY 1 AKLETYTLGNIGKRGRTVLVNPNGVNPPTGVASTSQAGVAPALEKVTVSQPSNRK 60  

DB 2 AKQQAATLISGKGGDVTLDINPBGVNPNGVVALSPAGVAPALEKVTTSVSQPSNRK 61  

QY 61 NYKQVQVIONPACTANGSCDPSTVRKQVADVTFTSYSTDBERRAFVRETLALLAPL 120  

DB 62 NYKQVQVIONPSTASTAGTCDPSTVRASVDTFTSYSTVERRALVRETLQALLDPM 121  

QY 121 LIDAIIDQINPAY 132  

DB 122 LVNAIDMLNPAY 133  

  

RESULT 9  

COAT_BPSP STANDARD; PRT; 132 AA.  

AC P03673;  

DT 01-MAR-1989 (Rel. 10, Created)  

DT 01-MAR-1989 (Rel. 10, Last sequence update)  

DT 01-FEB-1994 (Rel. 28, Last annotation update)  

DE Coat protein.  

OS Bacteriophage SP.  

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  

OC Alloviriviruses.  

OX NCBI_TaxID=12027;  

RN [1]  

RN SEQUENCE FROM N.A.  

RP MEDLINE=88289362; PubMed=3399390;  

RX Hiraeshima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;  

RT "Analysis of the complete nucleotide sequence of the group IV RNA  

RT coliphage SP."  

RL Nucleic Acids Res. 16:6205-6221(1988).  

CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.  

CC  

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CC  

CC EMBL; X07489; CAA30374.1; -.  

CC HSSP; P03615; IOBE.

```


DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
DR CoRo; COG0000; Levi_coat; 1.
SQ SEQUENCE 132 AA; 14128 MW; 50B1E6CC6AFA0A254 CRC64;

Query Match 80.0%; Score 531.5; DB 1; Length 132;
Best Local Similarity 78.8%; Pred. No. 1.5e-43;
Matches 104; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 ALEETVTLGNIGKDGQTLVLPNGVPTNGVASTLSQAGAVPALERKRVTVSVQSPSRNRK 60
DB 2 AALNQVTLTKIGNGQTLTLTPRGVPTNGVASTLSBAGAVPALERKRVTVSVQSPSRNRK 61
QY 61 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120
DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 10
VAL_BPSP STANDARD; PRT; 331 AA.

AC P09677; 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Reactthrough protein A1 [contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allotetravirus.
NCBI_Taxid=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hiraehina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP."
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The reactthrough protein A1 includes the coat
protein sequence.

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CC EMBL; X07489; CAB37299.1; -.
DR PIR; S01964; S01964.
DR HSSP; P03615; 10BB.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KM Coat protein.
FT CHAIN 1 132 Coat protein.
FT CHAIN 1 331 Reactthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A6642B4B52C6582 CRC64;

Query Match 80.0%; Score 531.5; DB 1; Length 331;
Best Local Similarity 78.8%; Pred. No. 4.5e-43;
Matches 104; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLEETVTLGNIGKDGQTLVLPNGVPTNGVASTLSQAGAVPALERKRVTVSVQSPSRNRK 60
DB 2 AALNQVTLTKIGNGQTLTLTPRGVPTNGVASTLSBAGAVPALERKRVTVSVQSPSRNRK 61
QY 61 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120
DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120

DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 11
Q9TOR8 PRELIMINARY; PRT; 132 AA.

AC Q9TOR8; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allotetravirus.
NCBI_Taxid=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Root R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14703.1; -.
DR HSSP; P03615; 10BB.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KM Coat protein.

SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 75.2%; Score 499.5; DB 2; Length 132;
Best Local Similarity 75.8%; Pred. No. 1.9e-40;
Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 ALEETVTLGNIGKDGQTLVLPNGVPTNGVASTLSQAGAVPALERKRVTVSVQSPSRNRK 60
DB 2 AALNQVTLTKIGNGQTLTLTPRGVPTNGVASTLSBAGAVPALERKRVTVSVQSPSRNRK 61
QY 61 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120
DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKXADVTFSFTQSTDBERAFVTELAALIASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 12
O64310 PRELIMINARY; PRT; 330 AA.
AC O64310; 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC A10Levivirus.
 OX NCBI_TaxID=75725;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta."
 RL J. Mol. Biol. 247:903-917(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis."
 RL J. Mol. Biol. 256:8-19(1996).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF059243; AAC14704.1; -.
 DR HSSP: P03615; 108; C:Viral capsid; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR002703; Levi.coat.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF01819; Levi.coat.1.
 DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 961B55F408334410 CRC64;
 Query Match 75.4%; Score 499.5; DB 2; Length 330;
 Best Local Similarity 75.8%; Pred. No. 5.6e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKETVTLGNIGDGRQTLVLRGVNPTNGVSLSGAGVPALEKRYTVTSQPSNRK 60
 DB 2 AKNKTLTGTIGAGAGQTLTLTRGVNPTNGVSLSGAGVPALEKRYTVTSQPSNRK 61
 QY 61 NYKQVQKIONPTACTANGSCDPSVTROKVADYTFSPQYSTDEERAFVRELAALASPL 120
 DB 62 NYKQVQKIONPTACTANGSCDPSVTROKVADYTFSPQYSTDEERAFVRELAALASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 TVDAIDQLNPAY 132
 RESULT 13
 COAT_BPERR STANDARD; PRT; 131 AA.
 ID COAT_BPERR STANDARD; PRT; 131 AA.
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OX unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC - FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR InterPro: IPR002703; Levi.coat.
 DR Pfam: PF01819; Levi.coat.1.
 KW Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B59E1E50FC612 CRC64;

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0028;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTLVLRGVNPT-----NGVASLSQAGVPALEKRYTVTSQPSNRKRYKQV 66
 DB 4 QNLVLRDREATPDHTEFVRDIRDNGEVEESVIGSFRTISRTKTSNGR--YKSTL 61
 QY 67 KIONPT--ACTANGSCDPSVTROKVADYTFSPQYSTDEERAFVRELAALASPLI- 122
 DB 62 KLVVPVQSGQTVNGIYTPVVRKISYTVDPDARSTTERNNFVGMIDALKADMLVH 121
 QY 123 DAIDQLNPAY 132
 DB 122 DTIVNLQGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Tmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=2235095; PubMed=12461651;
 RA Kiss H., Darai E., Kiss C., Kost-Alimova M., Klein G., Dumaneki J.P.,
 RA Iren S.;
 RT "Comparative human/murine sequence analysis of the common eliminated
 RT region 1 from human 3p21.3."
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL: AJ248064; CAD20986.1; -.
 DR MGD: MGI:2446841; Tmem7.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0E69F2A4D CRC64;
 Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.96;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;
 QY 5 TVTLGNIGDGRQTLV-----LNRGVNPTNG--VASLSQAGVPALEKRYK 46
 DB 195 TATCSNISSQSPSSKQVMPQASKAPQASNPFTKNDKVCSTKRPAPLSPTSLKARBP 254
 QY 47 RYTVSVSQPSNRKRYKQV-----KIONPT-----ACTANGSCDPSVTRO----- 87
 DB 255 KYTVCSNISSRSKSKQVMPQASKVPQTSNPTKNDPKISCSKSTPRLTIQQLSVV 314
 QY 88 -----KYADVTFSPQYSTDEERAFVRELAALASPLI 122
 DB 315 SPAPAPTCVIQMPSPPTIDGSRADVAKENTRSKTPK-----ALLSPLYV 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P1830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeriolysin precursor (Thiol-activated cytolysin).
 GN Name=Isc; seeligeri.
 OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

```

OX NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SLCC;
RX MEDLINE=92182018; Pubmed=1543752;
RA Haas A., Dumbsky M., Kreft J.;
RT "Listeriolysin genes: complete sequence of ilo from Listeria ivanovi
and of ilo from Listeria seeligeri.";
RL Biochim. Biophys. Acta 1130:81-84(1992).
-1- FUNCTION: Sulfhydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
Cholesterol is the receptor for the binding of these toxins to
eukaryotic cell membranes.
-1- SIMILARITY: Belongs to the thiol-activated cytolysin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL; X60462; CAA42996.1; -.
DR PIR; S22340; S22340.
DR HSSP; P19995; 1PFO.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PRO1400; TACTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOLE_CYTOLYSINS; 1.
KW Cytolysin; Hemolysis; Lipid-binding; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 530
FT SITE 485 485
FT SEQUENCE 530 AA; 59181 MW; 416F7A4DD2029866 CRC64;
SQ
Query Match 13.5%; Score 89.5; DB 1; Length 530;
Best Local Similarity 25.0%; Pred. No. 5.2;
Matches 34; Conservative 22; Mismatches 37; Indels 43; Gaps 7;
QY 13 KGRQTLVL--NPRGVNPT-----NGVASLSQAG-----VPALEKRV 48
DB 94 KQGESEYIVVEKKKKKGINNNADISVINAISSLTYPGALVYRANRELVENQPNVLPVXRDSL 153
QY 49 TVSVSQPSRRKRYKQVKTQNTACTANGSCDPSVTR--QKY-----ADVTFSFTQ 98
DB 154 TLSVDLPGMTKDKNKFVK--NPTKSNVNNVAVTLVERWMDKYSKAVPINAKIDYS--- 208
QY 99 YSTDERAFVTELA 114
DB 209 ----DEMAVSESQLIA 220

```

Search completed: January 4, 2005, 09:16:17
Job time : 37.2676 secs

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OM protein - protein search, using bw model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-8

Perfect score: 664
Sequence: 1 ALEFWTLGNIGRDKQTLV.....AALLASPLILDAIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: A_Geneseq_23Sep04:*
 - 2: geneseqp1980a:*
 - 3: geneseqp1990a:*
 - 4: geneseqp2000a:*
 - 5: geneseqp2001a:*
 - 6: geneseqp2002a:*
 - 7: geneseqp2003a:*
 - 8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	664	100.0	132	5	ABG94318	Abg94318 POB250 pr
2	664	100.0	132	5	ABG80630	Abg80630 Bacteriop
3	664	100.0	132	6	ABR56454	AbR56454 Bacteriop
4	664	100.0	132	6	ABU09691	Abu09691 Bacteriop
5	664	100.0	132	6	ABR44557	AbR44557 Bacteriop
6	664	100.0	132	7	ADD24132	Add24132 Bacteriop
7	664	100.0	132	7	ADJ82058	Adj82058 Protein f
8	664	100.0	132	7	ADK17146	Adk17146 Virus-11k
9	664	100.0	132	8	ADJ36315	Adj36315 Bacteriop
10	664	100.0	132	8	ADU67161	AdU67161 Phage Qbe
11	664	100.0	132	8	ADK52195	Adk52195 Bacteriop
12	661	99.5	132	5	ABG94316	Abg94316 POB240 pr
13	661	99.5	132	5	ABG80628	Abg80628 Bacteriop
14	661	99.5	132	6	ABR56452	AbR56452 Bacteriop
15	661	99.5	132	6	ABU09689	Abu09689 Bacteriop
16	661	99.5	132	6	ABR44555	AbR44555 Bacteriop
17	661	99.5	132	7	ADD24130	Add24130 Bacteriop
18	661	99.5	132	7	ADJ82056	Adj82056 Protein f
19	661	99.5	132	7	ADK17144	Adk17144 Virus-11k
20	661	99.5	132	8	ADJ36313	Adj36313 Bacteriop
21	661	99.5	132	8	ADU67159	AdU67159 Phage Qbe
22	661	99.5	132	8	ADK52193	Adk52193 Bacteriop
23	658	99.1	132	5	ABG94319	Abg94319 POB250 pr
24	658	99.1	132	5	ABG80631	Abg80631 Bacteriop
25	658	99.1	132	6	ABR56456	AbR56456 Bacteriop

26	658	99.1	132	6	ABU09692	Abu09692 Bacteriop
27	658	99.1	132	6	ABR44559	AbR44559 Bacteriop
28	658	99.1	132	7	ADD24134	Add24134 Bacteriop
29	658	99.1	132	7	ADJ82060	Adj82060 Protein f
30	658	99.1	132	7	ADK17148	Adk17148 Virus-11k
31	658	99.1	132	8	ADJ36317	Adj36317 Bacteriop
32	658	99.1	132	8	ADU67163	AdU67163 Phage Qbe
33	655	98.6	132	8	ADK52197	Adk52197 Bacteriop
34	655	98.6	132	5	ABG94320	Abg94320 POB251 pr
35	655	98.6	132	5	ABG80632	Abg80632 Bacteriop
36	655	98.6	132	6	ABR56455	AbR56455 Bacteriop
37	655	98.6	132	6	ABU09693	Abu09693 Bacteriop
38	655	98.6	132	6	ABR44558	AbR44558 Bacteriop
39	655	98.6	132	7	ADD24133	Add24133 Bacteriop
40	655	98.6	132	7	ADJ82059	Adj82059 Protein f
41	655	98.6	132	7	ADK17147	Adk17147 Virus-11k
42	655	98.6	132	8	ADJ36316	Adj36316 Bacteriop
43	655	98.6	132	8	ADU67162	AdU67162 Phage Qbe
44	655	98.6	132	8	ADK52196	Adk52196 Bacteriop
45	652	98.2	132	5	ABG94233	Abg94233 Bacteriop

ALIGNMENTS

RESULT 1
ID ABG94318 standard; protein; 132 AA.
XX
AC ABG94318;
XX
DT 29-AUG-2003 (revised)
DT 10-DEC-2002 (first entry)
XX
DE POB250 protein.
XX
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
XX cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;
XX vaccine; infectious disease.
XX
OS unidentified bacteriophage.
XX
PN W0200256905-A2.
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002W0-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326988P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Renner WA, Bachmann M, Tisot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX WPI; 2002-627351/67.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Claim 18; Page 145; 441pp; English.
XX
XX This invention relates to a novel ordered and repetitive antigen array
XX used in the production of vaccines for infectious diseases. The invention
XX also discloses a composition comprising a non-natural molecular scaffold
XX comprising a core particle selected from a core particle of a non-natural
XX origin and a core particle of natural origin and an organism comprising
XX at least one first attachment site, where the organism is connected to
XX the core particle by at least one covalent bond. Also disclosed is an
XX antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abetal-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGAGVAPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGAGVAPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIONPTACTANGSCDPSVTQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
 DB 61 NYKVQVKIONPTACTANGSCDPSVTQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 2
 ABG80630
 ID ABG80630 standard; protein; 132 AA.

XX ABG80630;
 AC 29-NOV-2002 (first entry)
 DB Bacteriophage Q-beta A1 coat protein mutant Qbeta-250.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

XX Bacteriophage Qbeta.
 OS Synthetic.

XX MO200256907-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002MO-IB000168.

PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326988P.
 PR 07-NOV-2001; 2001US-0331045P.

XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVA) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEB) LUEBEND R.
 PA (STAUF) STAUFENBIEL M.
 PA (FREY) FREY P.
 PI Maurer P, Lechner F, Ortmann R, Luecend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 DR WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

PS Example 18; Page 145; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site (Abeta 1-42) or its fragment, and where the second
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC Gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGAGVAPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGAGVAPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIONPTACTANGSCDPSVTQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
 DB 61 NYKVQVKIONPTACTANGSCDPSVTQKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 3
 ABR56454
 ID ABR56454 standard; protein; 132 AA.

XX ABR56454;
 AC 28-JUL-2003 (first entry)
 DT Bacteriophage Q-beta coat protein mutant SEQ ID NO:25.
 DE
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KM cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 KM antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KM antithyroid; antidiabetic; neuroprotective; nootropic; osteoplastic;
 KM antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KM inflammatory autoimmune disease.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX WO2003024480-A2.
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-IB004252.
 PF 14-SEP-2001; 2001US-0318967P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann MF, Storni T, Lechner F,
 PI WPI; 2003-363095/34.
 DR A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumours or infectious diseases, e.g. viral
 PT infections.
 XX
 PS Disclosure; Page 181; 243pp; English.
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antineumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC65838 to ACC65852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLEVTTLNIGRDGQTLVLPNGVPTNGVASTLSQAGAVPALERKVTVSQPSRNRK 60

DB 1 ARLEVTTLNIGRDGQTLVLPNGVPTNGVASTLSQAGAVPALERKVTVSQPSRNRK 60
 QY 61 NKKVQVKIONPTACTANGSCDPSVTRQKYADYTFSPFOYSTDEERAFVTELAALASPL 120
 DB 61 NKKVQVKIONPTACTANGSCDPSVTRQKYADYTFSPFOYSTDEERAFVTELAALASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 RESULT 4
 ABU09691
 ID ABU09691 standard; protein; 132 AA.
 XX
 AC ABU09691;
 XX
 DT 03-JUL-2003 (first entry)
 XX
 DE Bacteriophage Qbeta mutant coat protein #3.
 XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KM cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KM renin-activated angiotensin system; hypertension; stroke; infarction;
 KM congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KM mutein.
 XX Bacteriophage Qbeta.
 OS WO2003031466-A2.
 XX 17-APR-2003.
 PD 07-OCT-2002; 2002WO-BE011219.
 PF 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann M;
 PI WPI; 2003-430264/40.
 DR New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX Claim 20; Page 94; 97pp; English.
 XX The invention describes an angiotensin peptide moiety carrier conjugate
 CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC mutant bacteriophage Qbeta coat protein used in the preparation of the
 CC vaccine conjugates of the invention
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETTIGNIGDQKOTLVNPRGVNPTNGVASLSQAQAVPALERKRVTVSVSOPSRNRK 60
 DB 1 ARLETTIGNIGDQKOTLVNPRGVNPTNGVASLSQAQAVPALERKRVTVSVSOPSRNRK 60

QY 61 NYKVQKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120
 DB 61 NYKVQKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120

QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 5
 ABR44557
 ID ABR44557 standard; protein; 132 AA.

AC ABR44557;
 XX
 DT 25-JUL-2003 (first entry)

XX Bacteriophage Q-beta coat protein mutant SEQ ID NO:25.
 XX
 XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytotoxic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX Bacteriophage Qbeta.
 OS Synthetic.
 XX
 XX WO2003024481-A2.
 PN
 XX
 XX 27-MAR-2003.
 PD
 XX
 XX 16-SEP-2002; 2002WO-IB004132.
 PF
 XX
 XX 14-SEP-2001; 2001US-0318994P.
 PR
 XX 22-APR-2002; 2002US-0374145P.
 PR
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR/) MAURER P.
 PA (TISSE/) TISSOT A.
 PA (SCHW/) SCHWARZ K.
 PA (WEID/) WEIJERINK E.
 PA (LIP/) LIPOWSKY G.
 PA (PUM/) PUMPENS P.
 PA (CIEL/) CIELENS I.
 PA (RENN/) RENHOFFA R.
 XX
 XX Maurer P, Tisseot A, Schwarz K, Weijerink E, Lipowsky G,
 PI Pumpens P, Cielems I, Renhoffs R, Bachmann MF, Storni T;
 XX
 XX WPI; 2003-354564/33.
 DR
 XX
 XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 XX Disclosure; Page 260-261; 322pp; English.
 PS
 XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC creating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention

XX Sequence 132 AA;
 SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETTIGNIGDQKOTLVNPRGVNPTNGVASLSQAQAVPALERKRVTVSVSOPSRNRK 60
 DB 1 ARLETTIGNIGDQKOTLVNPRGVNPTNGVASLSQAQAVPALERKRVTVSVSOPSRNRK 60

QY 61 NYKVQKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120
 DB 61 NYKVQKIONPRACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120

QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 6
 ADD24132
 ID ADD24132 standard; protein; 132 AA.
 XX
 XX ADD24132;
 AC
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX
 XX Bacteriophage Qbeta coat protein mutant Qbeta-250.
 DE
 XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; coat protein; mutant; mutin.
 XX
 XX Synthetic.
 OS Bacteriophage Qbeta.
 XX
 XX WO2003059386-A2.
 PN
 XX
 XX 24-JUL-2003.
 PD
 XX
 XX 17-JAN-2003; 2003WO-EB000460.
 PF
 XX
 XX 18-JAN-2002; 2002US-00050902.
 PR
 XX 21-JAN-2002; 2002WO-IB000166.
 PR
 XX 08-JUL-2002; 2002US-0393725P.
 PR
 XX 18-JUL-2002; 2002US-0396590P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M, Maurer P, Fellicioli E, Renner WA;
 PI WPI; 2003-598483/56.
 XX
 XX A vaccine composition for preventing or treating prion diseases (e.g.

PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

PS Example 1, SEQ ID NO 25, 246bp, English.

XX This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (Prp) or its dimer, or a Prp peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is the amino acid sequence of a mutant coat protein from Bacteriophage Qbeta which may be used during the creation of the vaccine composition of the invention.

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKVVQVKIONPFRCTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
DB 61 NKVVQVKIONPFRCTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 7

ADJ82058
ID ADJ82058 standard; protein; 132 AA.

AC ADJ82058;
XX
DT 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

XX osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.

XX Unidentified.

XX WO2003039225-A2.

XX 15-MAY-2003.

XX 07-NOV-2002; 2002WO-EP012449.

XX 07-NOV-2001; 2001US-0331045P.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-IB000166.

XX 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-441430/41.

PT New compositions comprising a core particle and at least one antigen or
PT antigenic determinant; useful for as a vaccine for therapy or prophylaxis
PT of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 25, 222bp; English.

XX The invention relates to a composition comprising a core particle having
CC at least one first attachment site, and at least one antigen or antigenic
CC determinant having at least one second attachment site. The antigen or
CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
CC peptide. The second attachment site is (non-) naturally occurring with
CC the antigen or antigenic determinant, and is capable of association to
CC the first attachment site. The antigen or antigenic determinant and the
CC core particle interact through the association to form an ordered and
CC repetitive antigen array. The composition is useful as a medicament, or
CC for the manufacture of a medicament for treating bone diseases. The
CC composition is especially useful for as a vaccine for therapy or
CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
CC and for stimulating mammalian immune system. This sequence represents a
CC protein of the invention.

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKVVQVKIONPFRCTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
DB 61 NKVVQVKIONPFRCTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 8

ADK17146
ID ADK17146 standard; peptide; 132 AA.

AC ADK17146;

DT 06-MAY-2004 (first entry)

DE Virus-like particle repetitive antigen array peptide #25.

XX anti-allergic; antiasthmatic; cytostatic; vaccine; virus-like particle;

KW interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;

XX allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

XX WO2003040164-A2.

XX 15-MAY-2003.

XX 07-NOV-2002; 2002WO-EP012455.

XX 07-NOV-2001; 2001US-0331045P.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-IB000166.

XX 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Jennings G, Sonderregger I;

XX WPI; 2003-441518/41.

PT Composition comprising an ordered and repetitive antigen or antigenic
PT determinant array; useful as a medicament, or for manufacturing a
PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's lymphoma.
XX
PS Disclosure; SEQ ID NO 25; 245pp; English.
XX
XX The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL)-5, IL-13 or ectaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or ectaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments, or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSQPSRNK 60
DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSQPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
QY 121 LIDAIIDQLNPAY 132
DB 121 LIDAIIDQLNPAY 132

RESULT 9
ADJ36315
ID ADJ36315 standard; protein; 132 AA.
XX
AC ADJ36315;
XX
DT 22-APR-2004 (first entry)
XX
XX Bacteriophage Qbeta coat protein virus-like particle mutant M10K.
DE Bacteriophage Qbeta coat protein virus-like particle mutant M10K.
XX
XX anti-allergic; cytostatic; virucide; immunostimulant; vaccine;
KM immune response; virus-like particle; immunostimulatory; allergy; tumour;
KM chronic disease; chronic viral disease; bacteriophage Qbeta;
KM coat protein; VLP; adjuvant; mutant; mutein.
XX
OS Bacteriophage Qbeta.
XX
PN WO2004000351-A1.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-EP006541.
XX
PR 20-JUN-2002; 2002US-0389898P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Renner WA;
XX
DR WPI; 2004-108361/11.
XX
PT New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
PS Disclosure; SEQ ID NO 16; 252pp; English.
XX
XX The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
CC coat protein mutant, a virus like particle (VLP) that can be used in the
CC adjuvant of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSQPSRNK 60
DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSQPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
QY 121 LIDAIIDQLNPAY 132
DB 121 LIDAIIDQLNPAY 132

RESULT 10
ADJ67161
ID ADJ67161 standard; protein; 132 AA.
XX
AC ADJ67161;
XX
DT 06-MAY-2004 (first entry)
XX
XX Phage Qbeta coat protein mutant Qbeta 250 for antigen display array.
DE Phage Qbeta coat protein mutant Qbeta 250 for antigen display array.
XX
XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
KM antigenic array.
XX
OS Bacteriophage Qbeta.
XX
PN WO2004009124-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-EP007849.
XX
PR 19-JUL-2002; 2002US-0396638P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Fulurija A;
XX
DR WPI; 2004-132866/13.
XX
PT New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.
XX
PS Disclosure; SEQ ID NO 19; 175pp; English.
XX
XX The invention relates to a new composition comprising: (i) a core
CC particle with at least one first attachment site; and (ii) at least one
CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is shrelin or a shrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the shrelin or a
 CC shrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC Qbeta coat protein mutant which can be used as part of the repetitive or
 CC antigenic array.

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRGKQTLVLPNGVPTNGVSLSQAGAVPALERKRVTVSVSQPSRNK 60

DB 1 ARLEVTTLGNIGRGKQTLVLPNGVPTNGVSLSQAGAVPALERKRVTVSVSQPSRNK 60

QY 61 NYKVQVKIONPPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBERAFVRTLAALASPL 120

DB 61 NYKVQVKIONPPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBERAFVRTLAALASPL 120

QY 121 LIDAIQQLNPAY 132

DB 121 LIDAIQQLNPAY 132

RESULT 11

ADK52195

ID ADK52195 standard; protein; 132 AA.

AC ADK52195;

DT 20-MAY-2004 (first entry)

XX Bacteriophage Qbeta coat protein mutant K2R K13R.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

XX core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX coat protein; CP; mutant; mutein.

XX Bacteriophage Qbeta.

XX Synthetic.

OS Bacteriophage Qbeta.

XX Key

XX Misc-difference 2 Location/Qualifiers

XX FT Misc-difference 13 /note="Wild type Lys substituted by Arg"

XX FT /note="Wild type Lys substituted by Arg"

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI (NOVS) NOVARTIS PHARMA AG.

XX PI Bachmann MF, Tisot A, Ortman R, Luesend R, Staufenbiel M,

XX PI Frey P,

XX PI WPI, 2004-203731/19.

PT Composition comprising a core particle with at least one attachment site,

PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases

PT such as Alzheimer's disease.

XX Example 1; SEQ ID NO 19, 184pp; English.

XX The invention describes a novel composition comprising a virus-like core

XX particle with at least one attachment site, and an antigenic amyloid beta

XX 1-6 peptide. The new composition comprises a core particle with at least

XX one first attachment site; and at least one antigen or antigenic

XX determinant with at least one second attachment site, where the antigen

XX or antigenic determinant is a Amyloid beta 1-6 peptide, and where the

XX second attachment site comprises an attachment site not naturally

XX occurring with the antigen or antigenic determinant; or an attachment

XX site naturally occurring with the antigen or antigenic determinant. The

XX second attachment site is capable of association to the first attachment

XX site and the beta 1-6 peptide and the core particle interact through the

XX association to form an ordered and repetitive antigen array. The

XX composition is useful for the manufacture of a medicament for treating

XX Alzheimer's disease and related diseases. This is the amino acid sequence

XX of an RNA bacteriophage Qbeta coat protein mutant that can be used in the

XX preparation of the compositions and vaccines of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRGKQTLVLPNGVPTNGVSLSQAGAVPALERKRVTVSVSQPSRNK 60

DB 1 ARLEVTTLGNIGRGKQTLVLPNGVPTNGVSLSQAGAVPALERKRVTVSVSQPSRNK 60

QY 61 NYKVQVKIONPPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBERAFVRTLAALASPL 120

DB 61 NYKVQVKIONPPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBERAFVRTLAALASPL 120

QY 121 LIDAIQQLNPAY 132

DB 121 LIDAIQQLNPAY 132

RESULT 12

ABG94316

ID ABG94316 standard; protein; 132 AA.

AC ABG94316;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

XX PGB240 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

XX cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

OS unidentified bacteriophage.

XX WO200256905-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-1B000166.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326989P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Renner WA, Bachmann M, Tisot A, Maurer P, Lechner F, Sebbel P;

XX Plossek C;

XX WPI; 2002-627351/67.
 DR Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Claim 18; Page 144; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 132 AA:
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLETTVGNIGRDKQKTLINPGVNPNGVASTSGAGVAPLKERVTVSVQSPSNRK 60
 DB 1 AKLETVLGNIGRDKQKTLINPGVNPNGVASTSGAGVAPLKERVTVSVQSPSNRK 60
 QY 61 NYKVQVNIQNPACTANGSCDPSVTROKVDVTFESFYQSTDEBRARVRELAALLASPL 120
 DB 61 NYKVQVNIQNPACTANGSCDPSVTROKVDVTFESFYQSTDEBRARVRELAALLASPL 120
 QY 121 LIDALDQLNPAY 132
 DB 121 LIDALDQLNPAY 132
 RESULT 13
 ABG80628
 ID ABG80628 standard; protein; 132 AA.
 AC
 XX ABG80628;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 XX Bacteriophage Q-beta A1 coat protein mutant Qbeta-240.
 DE
 XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; Igs-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KM enterokinase; cysteine-containing linker.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-1B000168.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEO/) LUEOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Flosek C;
 PT WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Example 18; Page 144; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (i) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, Igs-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 CC
 XX
 SQ Sequence 132 AA:
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 Db 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 QY 61 NKVVQVKIONPFACTANGSCDPSVTRQKADVTFSTQYSTDBERAFVRTTELAALIASPL 120
 Db 61 NKVVQVKIONPFACTANGSCDPSVTRQKADVTFSTQYSTDBERAFVRTTELAALIASPL 120
 QY 121 LIDAIIDQLNPAY 132
 Db 121 LIDAIIDQLNPAY 132

RESULT 14
 ABR56452
 ID ABR56452 standard; protein; 132 AA.
 XX ABR56452;
 AC ABR56452;
 XX 28-JUL-2003 (first entry)
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:23.
 XX
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytotoxic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antihypertoid; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 XX Bacteriophage Qbeta.
 OS Synthetic.
 OS WO2003024480-A2.
 XX
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-18004252.
 PF 14-SEP-2001; 2001US-0318967P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann MF, Storni T, Lechner F;
 PI MPI; 2003-363095/34.
 XX
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX
 XX Disclosure; Page 179-180; 243pp; English.
 XX
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytotoxic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antihypertoid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antineumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an

CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 132 AA:
 SO
 Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 Db 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 QY 61 NKVVQVKIONPFACTANGSCDPSVTRQKADVTFSTQYSTDBERAFVRTTELAALIASPL 120
 Db 61 NKVVQVKIONPFACTANGSCDPSVTRQKADVTFSTQYSTDBERAFVRTTELAALIASPL 120
 QY 121 LIDAIIDQLNPAY 132
 Db 121 LIDAIIDQLNPAY 132

RESULT 15
 ABU09689
 ID ABU09689 standard; protein; 132 AA.
 XX ABU09689;
 AC ABU09689;
 XX 03-JUL-2003 (first entry)
 DE Bacteriophage Qbeta coat protein #1.
 XX
 XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 XX
 XX Bacteriophage Qbeta.
 OS
 XX WO2003031466-A2.
 XX
 XX 17-APR-2003.
 PD 07-OCT-2002; 2002WO-EP011219.
 PF 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-18000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M;
 PI MPI; 2003-430264/40.
 XX
 XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX
 XX Claim 20, Page 93-94; 97pp; English.
 XX
 XX The invention describes an angiotensin peptide moiety carrier conjugate

CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC mutant bacteriophage Qbeta coat protein used in the preparation of the
 CC vaccine conjugates of the invention
 XX
 SQ Sequence 132 AA;

Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	ARLEVTIGNIGRDKQTLVNPGRVNPPTNGVASLSQAGAVPALERKVTVSQPSRNRK	60
		:	
DB	1	AKLETVTIGNIGRDKQTLVNPGRVNPPTNGVASLSQAGAVPALERKVTVSQPSRNRK	60
		:	
QY	61	NYKVQVKIONPTACTANGSCDPSVTROKVDVTFSSFTQYSTDERAFVRTETLAALIASPL	120
DB	61	NYKVQVKIONPTACTANGSCDPSVTROKVDVTFSSFTQYSTDERAFVRTETLAALIASPL	120
QY	121	LIDAIIDQINPAY	132
DB	121	LIDAIIDQINPAY	132

Search completed: January 4, 2005, 09:11:01
 Job time : 39.6824 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 10.3622 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-8

Perfect score: 664
Sequence: 1 ARLEVTYICNIGRDGKQTLV.....AALLASPLIDAIIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	12.3	626	4 US-09-485-717-2	Sequence 2, Appl1
2	81.5	12.3	626	4 US-09-948-722-2	Sequence 2, Appl1
3	75	11.3	409	4 US-09-328-352-4249	Sequence 4249, Ap
4	71.5	10.8	818	4 US-09-252-991A-16691	Sequence 16691, A
5	71.5	10.8	916	4 US-09-252-991A-23637	Sequence 23637, A
6	70.5	10.6	502	4 US-09-270-767-44620	Sequence 44620, A
7	69.5	10.5	129	1 US-08-090-148-1	Sequence 1, Appl1
8	69	10.4	300	4 US-09-302-626B-182	Sequence 182, App
9	69	10.4	622	4 US-09-302-626B-185	Sequence 185, App
10	69	10.4	766	4 US-09-538-092-216	Sequence 216, App
11	69	10.4	1073	4 US-09-206-942-47	Sequence 47, Appl
12	69	10.4	1079	4 US-09-206-942-47	Sequence 47, Appl
13	68.5	10.3	381	4 US-09-198-452A-745	Sequence 745, App
14	68.5	10.3	383	3 US-09-045-186-2	Sequence 2, Appl1
15	68.5	10.3	384	3 US-08-232-144-4	Sequence 4, Appl1
16	68.5	10.3	384	2 US-08-555-268A-15	Sequence 15, Appl
17	68.5	10.3	384	3 US-09-200-673-15	Sequence 15, Appl
18	68.5	10.3	384	4 US-10-013-846-4	Sequence 4, Appl1
19	68.5	10.3	384	4 US-09-708-392-9	Sequence 9, Appl1
20	68.5	10.3	384	5 PCT-US93-05039-3	Sequence 3, Appl1
21	68.5	10.3	411	5 US-08-817-869-3	Sequence 3, Appl1
22	68.5	10.3	411	5 PCT-US95-14377-3	Sequence 3, Appl1
23	68.5	10.3	733	4 US-09-248-796A-16565	Sequence 16565, A
24	68	10.2	316	4 US-09-270-767-43925	Sequence 43925, A
25	68	10.2	316	4 US-09-270-767-59311	Sequence 59311, A
26	68	10.2	415	4 US-09-252-991A-29602	Sequence 29602, A
27	67.5	10.2	424	3 US-09-173-581-7	Sequence 7, Appl1

28	67.5	10.2	424	3 US-09-420-915-7	Sequence 7, Appl1
29	67.5	10.2	428	3 US-09-134-001C-2885	Sequence 2885, Ap
30	67.5	10.2	1328	3 US-08-781-891-76	Sequence 76, Appl
31	67.5	10.2	1328	4 US-09-618-166-76	Sequence 76, Appl
32	67	10.1	1322	4 US-09-328-352-6759	Sequence 6759, Ap
33	67	10.1	1322	4 US-09-976-594-41	Sequence 41, Appl
34	66.5	10.0	279	3 US-08-397-411-13	Sequence 13, Appl
35	66.5	10.0	398	6 5495001-9	Patent No. 5495001
36	66.5	10.0	915	4 US-09-206-942-35	Sequence 35, Appl
37	66.5	10.0	1220	4 US-09-206-942-28	Sequence 28, Appl
38	66.5	10.0	1222	4 US-09-206-942-37	Sequence 37, Appl
39	66.5	10.0	1226	4 US-09-206-942-26	Sequence 26, Appl
40	66.5	10.0	1228	4 US-09-206-942-34	Sequence 34, Appl
41	66	9.9	187	3 US-08-916-246-12	Sequence 12, Appl
42	66	9.9	187	4 US-09-949-186-12	Sequence 12, Appl
43	66	9.9	1036	2 US-08-720-484A-5	Sequence 5, Appl1
44	66	9.9	1036	3 US-08-953-822A-5	Sequence 5, Appl1
45	66	9.9	1036	4 US-09-398-239-5	Sequence 5, Appl1

ALIGNMENTS

```
RESULT 1
US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan
; APPLICANT: Hees, Jergen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862PUS
; CURRENT APPLICATION NUMBER: US/09/485,717
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2

Query Match          12.3%; Score 81.5; DB 4; Length 626;
Best Local Similarity 22.0%; Pred. No. 0.3;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPNVGVASLSQAA-----VPALEKRV 48
      |||:|:|
DB 138 KGNIEYIVKKKKKSIQNNADIQVNAISLTPALVKANSELVENOPDVLVPRDSL 197
QY 49 TVVSQPSNRKKYKQVIONPTACTANGSCDPSVTR-----OKYADVFSTGYSTD 102
      |||:|:|
DB 198 TLSIDIPGNTNODNKIVVK--NATKSNVNNAVTVLVERNKKYAAQVPRVS---AATDID 252
QY 103 EERAFVRIEIAA 114
      |||:|:|
DB 253 DEMAYGESQLIA 264

RESULT 2
US-09-948-722-2
; Sequence 2, Application US/09948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan H. E.
; APPLICANT: Hees, Jergen
; TITLE OF INVENTION: Tuberculosis Vaccine
```

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FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2
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Query Match 12.3%, Score 81.5; DB 4; Length 626;
Best Local Similarity 22.0%; Pred. No. 0.3;

Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

```
QY 13 RDGKQTLVLP-----NPRGVNPTNGVASLSQAG-----VPALKRV 48
DB 138 KDGEXYIVVEKKKSNQNNADIQVNAISLSTYFGLVKNSELVNPQDVLVKKRDSL 197
QY 49 TVSVSOPSRNRKXKQVQKIQNPACTANGSCDPSVTR-----QKADYTFSTQYSTD 102
DB 198 TLTSLDLEGMTQKQKIVK--NATKSNVNNAVNLVLRKNEKKAQAYPNVS---AKIDYD 252
QY 103 EERAFVTELA 114
DB 253 DEMAYSESOLIA 264
```

RESULT 3

US-09-328-352-4249
Sequence 4249, Application US/09328352

```
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249
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Query Match 11.3%, Score 75; DB 4; Length 409;
Best Local Similarity 25.2%; Pred. No. 1;

Matches 31; Conservative 19; Mismatches 51; Indels 22; Gaps 5;

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QY 13 RDGKQTLVLP-----GVNPTNGVASLSQAGAVPALERKRVTV--SVSOPSRNRKXKQV 65
DB 118 RGTGRLNANVVRNALSPAVNPVDGTP-----IAKPRQRLTIRLLAPKRTGSN--A 169
QY 66 VKIQNPACTANGSCDPSVTRQKXADYTFSTQYSTDEERAFVTELAALLASPLLDIAI 125
DB 170 IAVLRETFNNALVAVENTAKYSEITF-----EEVMSVKTIATLHMLKASKKOLDL 222
QY 126 DDL 128
DB 223 PDL 225
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RESULT 4
US-09-252-991A-16691
Sequence 16691, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16691
LENGTH: 818
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16691
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Query Match 10.8%, Score 71.5; DB 4; Length 818;
Best Local Similarity 31.4%; Pred. No. 8.7;

Matches 27; Conservative 9; Mismatches 27; Indels 23; Gaps 4;

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QY 1 ARLETTIGNIRDGKQTLVLPNGVNPNG-----VASL-----SQAGVPALEK 46
DB 607 ARLRGV--LSQLRDGSAAALRTTEGVNTRGAIWALGLVAAALPRTQAGEVAABAG 665
QY 47 RV-----TVSVSOPSRNRKXKQV 64
DB 666 RIALDDPAAALGDSHGERVRRYGV 691
```

RESULT 5

US-09-252-991A-23637
Sequence 23637, Application US/09252991A

```
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637
```

Query Match 10.8%, Score 71.5; DB 4; Length 916;
Best Local Similarity 22.9%; Pred. No. 10;

Matches 27; Conservative 17; Mismatches 53; Indels 21; Gaps 4;

```
QY 9 GNIRDG-----KOTLVNPTNGVASLSQAGAVPALERKRVTVS-----QP 55
DB 789 GLDGEGALRLRAIVQARRIDPFQGLAALPVGGILPALQMEDPAFGSLDQWVQA 848
QY 56 SRNRKXKQVQKIQNPAC--TANGSCDPSVTRQKXADYTFSTQYSTDEERAFVTR 110
DB 849 EERAFVTELAARERHPCSTIEANADCPUSADAGK-----PWTIPSDSATRWALRT 901
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RESULT 6

US-09-270-767-44620
Sequence 44620, Application US/09270767


```

      1  TOPOLOGY: NOT RELEVANT
      2  MOLECULE TYPE: PROTEIN
      3  ORIGINAL SOURCE:
      4  ORGANISM: VIRUS
      5  FEATURE:
      6  NAME/KEY: Coat protein from MS2-RNA
      7  LOCATION: Location 1 through 129 below
      8  LOCATION: represents entire MS2 coat
      9  LOCATION: protein in the published
     10  LOCATION: sequence.
     11  PUBLICATION INFORMATION:
     12  AUTHORS: Min Jou, W.; Hageman, G.;
     13  AUTHORS: Ysebaert, M.; Fiers, W.
     14  TITLE: Nucleotide sequence of the
     15  TITLE: gene coding for the
     16  JOURNAL: Nature
     17  VOLUME: 237
     18  PAGES: 82-88
     19  DATE: 1972
     20  US-08-090-148-1
     21
     22  Query Match
     23  Best Local Similarity 10.5%; Score 69.5; DB 1; Length 129;
     24  Matches 24; Conservative 16; Mismatches 43; Indels 13; Gaps 2.
     25
     26  QY 27 NPTNGVA-----SLSQGAVPALEKRVTVSVSPSHRKNKYQVKNQPTACTANGSC 80
     27  Db 24 NFANGVAMWISSNRQA-----YKTCVSRRSSAQNRKRTIKVEPKVATGVGSGVE 76
     28
     29  QY 81 DPSVTRKQKADVTFSTFYQSTDERAFVTELLALL 116
     30  Db 77 LPVAMRSYINMELTIPFATNSDCELIIVAMQGL 112
     31
     32  RESULT 8
     33  US-09-302-626B-182
     34  ; Sequence 182, Application US/09302626B
     35  ; Patent No. 6709660
     36  ; GENERAL INFORMATION:
     37  ; APPLICANT: Scalato, Enzo
     38  ; APPLICANT: Maigiani, Vega
     39  ; APPLICANT: Rappuoli, Rino
     40  ; APPLICANT: Pizze, Mariagrazia
     41  ; APPLICANT: Grandi, Guido
     42  ; TITLE OF INVENTION: Meningococcal Antigens
     43  ; FILE REFERENCE: CHIR0159
     44  ; CURRENT APPLICATION NUMBER: US/09/302,626B
     45  ; CURRENT FILING DATE: 1999-04-30
     46  ; PRIOR APPLICATION NUMBER: PCT/IB99/00103
     47  ; PRIOR FILING DATE: 1999-01-14
     48  ; NUMBER OF SEQ ID NOS: 195
     49  ; SOFTWARE: PatentIn Ver. 2.1
     50  ; SEQ ID NO 182
     51  ; LENGTH: 300
     52  ; TYPE: PRT
     53  ; ORGANISM: Artificial Sequence
     54  ; FEATURE:
     55  ; OTHER INFORMATION: Description of Artificial Sequence: papa
     56  US-09-302-626B-182
     57
     58  Query Match
     59  Best Local Similarity 10.4%; Score 69; DB 4; Length 300;
     60  Matches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7.
     61
     62  QY 10 NIGDGGKQTLVLRGVNPTNGVASLSQAGAV-----PALEKRYT 49
     63  Db 5 NVHRDGSQMDSEASAVRVT-GAASVSSABAFAFGFMAAFSVMALGVAAFSPAPASGII 63
     64
     65  QY 50 VSVSQSPSRNR-----KNYKQVYKIQNPTACTANGSCDPSVTRKQKADVTFSTFYQSTDE 103
     66  Db 64 ADKSAFAPNRQAQVILQTNANGLPQVNIQTPS-----SGQSVNRR-----PFOQFDVE 108

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EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 1079
TYPE: PR1
ORGANISM: Haemophilus influenzae
US-09-206-942-47

Query Match 10.4%; Score 69; DB 4; Length 1079;
Best Local Similarity 22.0%; Pred. No. 28;
Matches 27; Conservative 26; Mismatches 52; Indels 18; Gaps 4;

QY 4 EYTLNIGRDKQTLVLPNRG-----VNPTGVASLSQAGVPALEKRVTSVQ 54
DB 772 KTLTVGNV--SGTVTVTANRGLTLTAGSTINGNTVTSOSGEIGSVTGKTVSVTA 829
QY 55 PSRN---RKNYKQVQKIONPACTANGSCDPSVTRQKADVTFPSFYQSTDEERAFVTE 111
DB 830 TAGSLTVKGAQKINATEGTATLTAASSG---KLTTEASSNITSAGQGVDSAQDGSIAQ 885
QY 112 LAA 114
DB 886 ISA 888

RESULT 13
US-09-198-452A-745
Sequence 745; Application US/09198452A

PATENT NO. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 745
LENGTH: 381
TYPE: PR1
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: SITE
LOCATION: 1...381
OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-745

Query Match 10.3%; Score 68.5; DB 4; Length 381;
Best Local Similarity 19.8%; Pred. No. 6.2;
Matches 26; Conservative 27; Mismatches 63; Indels 15; Gaps 3;

QY 3 LETVTGNTGRDQKQTLVLPNRGVPNTNGVASLSQAGVPALEKRVTSVQSPSRNKNY 62
DB 6 VKTVIL-NIGRKTLQIGIKKKKIGISGLFLDLV-----LGVSGQRPETISANY 56
QY 63 KQVQKIONPACTANGSCDPSVTRQKADVTFPS-----FTQYSTDEERAFVTELAAL 116
DB 57 KHNLRDEKLAACPKNSAASLSAKKSHTKTTPGSIPEKSVSKPDATODKTFOKTSGSAPF 116
QY 117 ASPLLDIAID 127
DB 117 AKPTLKEEE 127

RESULT 14
US-09-045-186-2
Sequence 2; Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn

APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-045-186-2

Query Match 10.3%; Score 68.5; DB 3; Length 383;
Best Local Similarity 25.0%; Pred. No. 6.3;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRGVPNTN-----GVA---SLQAGVPALEKRVTSVQSPSRNKNYKQV 67
DB 138 RQQLINPGRMNNHAYGVIVVAVVAVASSLPFLIYQ--VTDEPRON----- 186
QY 68 IQNPACTANGSCDPSVTRQKADVTFPSFYQSTDEERAFVTELAAL 115
DB 187 -----VTLDAYDKVCFDQFSDSHRLSYTLVLVL 218

RESULT 15
US-08-232-144-4
Sequence 4; Application US/08232144

PATENT NO. 5571695
GENERAL INFORMATION:
APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 13th St, N.W., Suite 701-East
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,144
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-8

Perfect score: 664
Sequence: 1 ARLETTTGNIGRDGKQTLV.....AALLSPILDAIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	14	US-10-243-739-25
2	664	100.0	132	14	US-10-244-065-25
3	664	100.0	132	14	US-10-289-454-25
4	664	100.0	132	14	US-10-050-902-257
5	664	100.0	132	14	US-10-050-898-257
6	664	100.0	132	14	US-10-346-190-25
7	664	100.0	132	15	US-10-465-811-16
8	664	100.0	132	15	US-10-289-456-25
9	664	100.0	132	15	US-10-622-064-8
10	664	100.0	132	15	US-10-622-124-19
11	664	100.0	132	16	US-10-622-087-19
12	661	99.5	132	14	US-10-243-739-23
13	661	99.5	132	14	US-10-244-065-23

14	661	99.5	132	14	US-10-289-454-23	Sequence 23, App1
15	661	99.5	132	14	US-10-050-902-255	Sequence 255, App
16	661	99.5	132	14	US-10-050-898-255	Sequence 255, App
17	661	99.5	132	14	US-10-346-190-23	Sequence 23, App1
18	661	99.5	132	15	US-10-465-811-14	Sequence 14, App1
19	661	99.5	132	15	US-10-289-456-23	Sequence 23, App1
20	661	99.5	132	15	US-10-622-064-6	Sequence 6, App1
21	661	99.5	132	15	US-10-622-124-17	Sequence 17, App1
22	661	99.5	132	16	US-10-622-087-17	Sequence 17, App1
23	668	99.1	132	14	US-10-243-739-27	Sequence 27, App1
24	668	99.1	132	14	US-10-244-065-27	Sequence 27, App1
25	668	99.1	132	14	US-10-289-454-27	Sequence 27, App1
26	668	99.1	132	14	US-10-050-902-258	Sequence 258, App
27	668	99.1	132	14	US-10-050-898-258	Sequence 258, App
28	668	99.1	132	14	US-10-346-190-27	Sequence 27, App1
29	668	99.1	132	15	US-10-465-811-18	Sequence 18, App1
30	668	99.1	132	15	US-10-289-456-27	Sequence 27, App1
31	668	99.1	132	15	US-10-622-064-10	Sequence 10, App1
32	668	99.1	132	16	US-10-622-124-21	Sequence 21, App1
33	668	99.1	132	15	US-10-622-087-21	Sequence 21, App1
34	665	98.6	132	14	US-10-243-739-26	Sequence 26, App1
35	665	98.6	132	14	US-10-244-065-26	Sequence 26, App1
36	665	98.6	132	14	US-10-289-454-26	Sequence 26, App1
37	665	98.6	132	14	US-10-050-902-259	Sequence 259, App
38	665	98.6	132	14	US-10-050-898-259	Sequence 259, App
39	665	98.6	132	14	US-10-346-190-26	Sequence 26, App1
40	665	98.6	132	15	US-10-465-811-17	Sequence 17, App1
41	665	98.6	132	15	US-10-289-456-26	Sequence 26, App1
42	665	98.6	132	15	US-10-622-064-9	Sequence 9, App1
43	665	98.6	132	15	US-10-622-124-20	Sequence 20, App1
44	665	98.6	132	16	US-10-622-087-20	Sequence 20, App1
45	652	98.2	132	14	US-10-243-739-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-10-243-739-25
; Sequence 25, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornli, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243, 739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318, 967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 25
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-25

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLETTTGNIGRDGKQTLVLPNGVNPNGVNASLSQAGAVPLERKVVTVSVSQPSRNRK 60
DB 1 ARLETTTGNIGRDGKQTLVLPNGVNPNGVNASLSQAGAVPLERKVVTVSVSQPSRNRK 60
QY 61 NYVQVQKIONPACTANGSCDPSVTROKADYVTFSTQXSTDEBRAFVTELAALASPL 120
DB 61 NYVQVQKIONPACTANGSCDPSVTROKADYVTFSTQXSTDEBRAFVTELAALASPL 120
QY 121 LIDAIDQINPAY 132

Db 121 LIDAIQDLPAY 132

RESULT 2

US-10-244-065-25
; Sequence 25, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tisot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielems, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
; FILE REFERENCE: 1700.0230001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-25

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ARLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQYKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQYKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 3
US-10-289-454-25
; Sequence 25, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 25
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta-250
US-10-289-454-25

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ARLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQYKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQYKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 4

US-10-050-902-257
; Sequence 257, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 257
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-050-902-257

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKVTVSQPSRNRK 60
DB 1 ARLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQYKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQYKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

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RESULT 5
US-10-050-898-257
; Sequence 257, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tiseet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staudenfel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCES: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 257
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-050-898-257

Query Match
Best Local Similarity 100.0%; Score 664; DB 14; Length 132;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGRDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQSPSRNK 60
Db 1 ARLEVTTLGNIGRDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQSPSRNK 60
Qy 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Db 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 6
US-10-346-190-25
; Sequence 25, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCES: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
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; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-346-190-25

Query Match
Best Local Similarity 100.0%; Score 664; DB 14; Length 132;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGRDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQSPSRNK 60
Db 1 ARLEVTTLGNIGRDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQSPSRNK 60
Qy 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Db 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 7
US-10-465-811-16
; Sequence 16, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCES: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
US-10-465-811-16

Query Match
Best Local Similarity 100.0%; Score 664; DB 15; Length 132;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGRDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQSPSRNK 60
Db 1 ARLEVTTLGNIGRDGQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQSPSRNK 60
Qy 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Db 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 8
US-10-289-456-25
; Sequence 25, Application US/10289456
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PublicatIon No. US2004003321A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
PRIORITY FILING DATE: 2002-11-07
PRIORITY APPLICATION NUMBER: PCT/IB02/00166
PRIORITY FILING DATE: 2002-01-21
PRIORITY APPLICATION NUMBER: US 10/050,902
PRIORITY FILING DATE: 2002-01-18
PRIORITY APPLICATION NUMBER: US 60/396,635
PRIORITY FILING DATE: 2002-07-19
PRIORITY APPLICATION NUMBER: US 60/331,045
PRIORITY FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 250 mutant
US-10-289-456-25

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Query Match	100.0%	Score 664;	DB 15;	length 132;
Best Local Similarity	100.0%	Pred. No. 2,1e-66;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ARLEVTVLGNIGRGDQKQTLVLPNPGVNPFTNGVASISQAGAVPALEKRVTVSVSOPSRRNK	60	
Db	1	ARLEVTVLGNIGRGDQKQTLVLPNPGVNPFTNGVASISQAGAVPALEKRVTVSVSOPSRRNK	60	
QY	61	NYKQVKTQNTACTCANGSCDPSVTRQKADVTFSFTQYSNDERBAFRTTELAALLASPL	120	
Db	61	NYKQVKTQNTACTCANGSCDPSVTRQKADVTFSFTQYSNDERBAFRTTELAALLASPL	120	
QY	121	LIDAIIDQNPAY	132	
Db	121	LIDAIIDQNPAY	132	

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RESULT 9
US-10-622-064-8
; Sequence 8, Application US/106522064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrik F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 132
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
US-10-622-064-8

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Query Match 100.0%; Score 664; DB 15 Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 ARLEVTITAGTGRDGQIVLNPGRVNPINGVIALSLQACAVPALERVTVSQSPERRNK 60
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Db 1 AALEVTYTGNIGRDGKQGLTYLNPGRVNPPTNGVALISQAGVAPALAEKEVTYSVQPSNRK 60

Qy 61 NKVKVKIKIONPACTRANGSCDPSVTRCKKAAVTESFYQYSTDEBRAVVRTELAAALASPL 120

Db 61 NKVKVKIKIONPACTRANGSCDPSVTRCKKAAVTESFYQYSTDEBRAVVRTELAAALASPL 120

Qy 121 LIDAIIDQLNPAY 132

Db 121 LIDAIIDQLNPAY 132

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, RESULT 10
, US-10-622-124-19
, Sequence 19, Application US/10622124
, Publication NO. US20040076645A1
, GENERAL INFORMATION:
, APPLICANT: Bachmann, Martin F
, APPLICANT: Falturija, Alma
, TITLE OF INVENTION: Ghrelin-Carrier Conjugates
, FILE REFERENCE: 1700.0340001
, CURRENT APPLICATION NUMBER: US/10/622,124
, CURRENT FILING DATE: 2003-07-18
, PRIOR APPLICATION NUMBER: US 60/396,638
, PRIOR FILING DATE: 2002-07-19
, NUMBER OF SEQ ID NOS: 146
, SOFTWARE: PatentIn version 3.2
, SEQ ID NO 19
, LENGTH: 132
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
, US-10-622-124-19

```

	Query March Best Local Similarity	100.0%; 100.0%	Score 664; Pred. No. 2.1e-66;	DB 15; 1.0e-66;	Length 132; 1.0e-66;	Mismatches 0; 0;	Indels 0; 0;	Gaps 0; 0;
QY	1 ARLETTVLGNIGRDKQTLVILNPRGVPTNGVASLSQGAVPALAEKRYTVSVSOPSRNRK	60						
DB	1 ARLETVTLGNIGRDKQTLVILNPRGVPTNGVASLSQGAVPALAEKRYTVSVSOPSRNRK	60						
QY	61 NYKYQYKIQNPACTNGSCDPSVTRKQKADVTFSFTQYSTDDEBAFVETLALLASPL	120						
DB	61 NYKYQYKIQNPACTNGSCDPSVTRKQKADVTFSFTQYSTDDEBAFVETLALLASPL	120						
QY	121 LIDALDQLNPAY	132						
DB	121 LIDALDQLNPAY	132						

```

, RESULT 11
, US-10-622-087-19
, Sequence 19, Application US/10622087
, Publication No. US20040141984A1
, GENERAL INFORMATION:
, APPLICANT: Bachmann, Martin F
, APPLICANT: Tissot, Alain
, APPLICANT: Ortman, Rainer
, APPLICANT: Luond, Rainer
, APPLICANT: Staufenbiel, Matthias
, APPLICANT: Frey, Peter
, TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
, FILE REFERENCE: 1700.0350002
, CURRENT APPLICATION NUMBER: US/10/622,087
, CURRENT FILING DATE: 2003-07-18
, PRIOR APPLICATION NUMBER: US 60/396,639
, PRIOR FILING DATE: 2002-07-19
, PRIOR APPLICATION NUMBER: US 60/470,432
, PRIOR FILING DATE: 2003-05-15
, NUMBER OF SEQ ID NOS: 93
, SOFTWARE: PatentIn version 3.2
, SEQ ID NO 19

```


LENGTH: 132
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
US-10-622-087-19

Query Match 100.0%; Score 664; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 2, 1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
DB 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
QY 61 NYVQVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYVQVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 12
US-10-243-739-23
Sequence 23, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornl, Tazio
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 132
TYPE: PRF
ORGANISM: Bacteriophage Q-beta
US-10-243-739-23

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4, 5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
DB 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
QY 61 NYVQVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYVQVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 13
US-10-244-065-23
Sequence 23, Application US/10244065
Publication No. US2003009668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornl, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tisot, Alain

APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Clejens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 132
TYPE: PRF
ORGANISM: Bacteriophage Q-beta
US-10-244-065-23

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4, 5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
DB 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
QY 61 NYVQVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYVQVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 14
US-10-289-454-23
Sequence 23, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 132
TYPE: PRF
ORGANISM: Bacteriophage Q-beta-240
US-10-289-454-23

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4, 5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETTLGNIGDQKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60

```
Db      1 AKLETVTLGNIGRDGKQTLVLRGVNPTNGVSLSQAGAVPALKKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRTETLAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRTETLAALLASPL 120
QY      121 LIDAIQOLNPAY 132
Db      121 LIDAIQOLNPAY 132
```

RESULT 15

```
US-10-050-902-255
; Sequence 255, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 132
; TYPE: PRT
; ORGANISM: QB 240
US-10-050-902-255
```

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Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ARLETVTLGNIGRDGKQTLVLRGVNPTNGVSLSQAGAVPALKKRVTVSVSQPSNRK 60
Db      1 AKLETVTLGNIGRDGKQTLVLRGVNPTNGVSLSQAGAVPALKKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRTETLAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRTETLAALLASPL 120
QY      121 LIDAIQOLNPAY 132
Db      121 LIDAIQOLNPAY 132
```

Search completed: January 4, 2005, 09:41:22
Job time : 32.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-8

Perfect score: 664

Sequence: 1 ARLEVTTLGNIGRDKQTLV.....ALLASPLLDALDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	652	98.2	132	1	VCBPOB
2	526.5	79.3	331	1	S01964
3	116	17.5	131	1	VCBPP1
4	87.5	13.2	530	2	S22340
5	85.5	12.9	540	2	T00646
6	81.5	12.3	529	2	S24231
7	81.5	12.3	529	2	A43505
8	81.5	12.3	529	2	AC1100
9	81	12.2	830	2	S57537
10	80.5	12.1	1502	1	RGBYH1
11	77.5	11.7	528	2	S22341
12	77	11.6	432	2	T31660
13	76.5	11.5	136	2	C98821
14	76.5	11.5	136	2	AE3065
15	76.5	11.5	1052	2	C64221
16	76.5	11.5	1861	1	T13845
17	76	11.4	130	1	A46324
18	76	11.4	282	2	A10186
19	75.5	11.4	1097	2	AD2572
20	75	11.3	130	1	VCBPA
21	74.5	11.2	130	1	VCBPPR
22	74.5	11.2	161	4	I55480
23	74	11.1	340	2	S18650
24	74	11.1	340	2	A42008
25	73.5	11.1	520	1	ACMSD1
26	73.5	11.1	601	2	A55921
27	73.5	11.1	719	2	T39271
28	73	11.0	243	1	VHVPPT
29	73	11.0	430	2	G88884

30	72.5	10.9	129	1	VCBPP2	coat protein - pha
31	72.5	10.9	129	1	VCBPP7	coat protein - pha
32	72.5	10.9	129	1	VCBPPR	coat protein - pha
33	72	10.8	248	2	A86786	conserved hypotet
34	72	10.8	366	2	F70618	probable putA pro
35	72	10.8	1461	2	E90696	hypothetical prote
36	72	10.8	1461	2	A85547	hypothetical prote
37	71.5	10.8	293	2	F83618	conserved hypotet
38	71.5	10.8	439	2	T43813	translation elonga
39	71.5	10.8	458	2	T49114	hypothetical prote
40	71	10.7	376	2	C84316	hypothetical prote
41	71	10.7	399	1	A43685	polymerase-associ
42	71	10.7	463	2	S00676	translation elonga
43	70.5	10.6	191	2	H90078	hypothetical prote
44	70.5	10.6	654	2	S69673	SAC7 protein - yea
45	70	10.5	1545	2	T42751	sulfonylurea recep

ALIGNMENTS

RESULT 1

VCBPOB
coat protein - phage Q-beta

C/Species: phage Q-beta

C/Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004

C/Accession: A92240; A92221; A92088; A04224

R/Escarria, C.; Sastry, P.A.; Biller, M.A.

J. Biol. Chem. 253, 8390-8399, 1978

A/Title: Determination of the first half of the coat protein cistron of bacteriophage Qbe

A/Reference number: A92240; NCID:77118576; PMID:838709

A/Accession: A92240

A/Molecule type: mRNA

A/Residues: 1-80 <ES>

A/Cross-references: UNIPROT:P03615

R/Stoll, E.; Wilson, K.V.; Reiser, J.; Weismann, C.

J. Biol. Chem. 252, 990-993, 1977

A/Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.

A/Reference number: A92221, NCID:77118576; PMID:838709

A/Accession: A92221

A/Molecule type: protein

A/Residues: 1-60 <STO>

R/Maita, T.; Konigsberg, W.

J. Biol. Chem. 246, 5003-5024, 1971

A/Title: The amino acid sequence of the Qbeta coat protein.

A/Reference number: A92088; NCID:71288580; PMID:5570434

A/Accession: A92088

A/Molecule type: protein

A/Residues: 1-21, 'D', '23-55, 132 <MAI>

C/Superfamily: phage GA coat protein

Query Match 98.2%; Score 652; DB 1; Length 132;

Best Local Similarity 97.7%; Pred. No. 5.2e-57; Mismatches 1; Indels 0; Gaps 0;

Matches 129; Conservative 2;

Qy	1	ARLEVTTLGNIGRDKQTLVLPNGVPTNGVATSLQAGVPALEKRVTVSVSQPSNRK	60
Db	1	AKLEVTTLGNIGRDKQTLVLPNGVPTNGVATSLQAGVPALEKRVTVSVSQPSNRK	60
Qy	61	NYKVQVQIONPACTANGSCDPSVTROKTAADVTFSTQYSTDEERAFVTELAALLASPL	120
Db	61	NYKVQVQIONPACTANGSCDPSVTROKTAADVTFSTQYSTDEERAFVTELAALLASPL	120
Qy	121	LIDALDQNLNPAY 132	
Db	121	LIDALDQNLNPAY 132	

RESULT 2

S01964
readthrough protein - phage SP

C/Species: phage SP

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S01964
C/Inokuchi, Y.; Jacobson, A. B.; Hirose, T.; Inayama, S.; Hiraeshima, A.
Nucleic Acids Res. 16, 6205-6221, 1988
A/Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP
A/Reference number: S01963; PMID:88289362; PMID:3399390
A/Accession: S01964
A/Status: Preliminary
A/Molecule type: genomic RNA
A/Residues: 1-331 <INO>
A/Cross-references: UNIPROT:P09677; EMBL:X07489
A/Note: the authors translated the readthrough stopcodon TGA for residue 133 as Trp
A/Superfamily: phage GA coat protein

Query Match	79.3%	Score 526.5	DB 2	Length 331
Best Local Similarity	77.3%	Pred. No. 3.5e+44		
Matches 102	Conservative 14	Mismatches 15	Indels 1	Gaps 1

Qy 1 ARLEVTLTGNGRDRQOTLVNPRGVNPTNGVASLSQAGAVPALERKRVTSVSDPSRRK 60
 2 AKNQVTLTKIGKNGDQTLTLPGRVPTNGVASLSQAGAVPALERKRVTSVSDPSRRK 61

```

QY      61 NYKQVQKIQNPACANGSCDPSVRQKQADVTFSFTQYSTEEBARAFRTETLALLLPL 1200
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      62 NFKQIKLQNPACTRD-ACDPSVTRSAFADVTLSFTSYSTDEERALLRTETLALLLADPL 1200

```

```
Qy      121 L1DAIDQLNPAY 132
Db      121 IVD AIDNLNPAY 132
```

RESULT 3
VCBP1
coat protein - phage PR1
C/Species: phage PR1
C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C/Accession: A04225
C/Dnaase, P./ Vandekerckhove, J.S.; Van Montagu, M.C.
Eur. J. Biochem. 94, 375-386, 1979
A/Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage phi-X174
A/Reference number: A04225; MUID:79148387; PMID:107028

A1:Molecule type: protein
A1:Residues: 1-131 <DHA>
A1:Cross-references: UNIPROT:P03616
C1:Superfamily: phage GA coat protein

Query Match	17.5%;	Score 116;	DB 1;	Length 131;
Best Local Similarity	32.3%;	Pred. No. 0.00031;		
Matches 42;	Conservative 14;	Mismatches 58;	Indels	

Qy 17 QTVLTPGCVNPT-----NGVASLSQAGVPALEGRVTVSVS QPSRNRRKYKVG 66
Db 4 QNVLKQREATPNDHTFVPRDIRNVGEVESTGVPIGSRFTLSLRKTSNGR--YKSTLL 61

Dy 67 KIQNPT--ACTANGCDPSVTRQKADVTFSFTQYSDEER-AFVRRLAALLASPLLI-
| : | : | | | | | : | : | | | : | :
Db 62 KLIVPVVGSGTUNGIVTPVVYRTSYTVDFDYDARSTTKERNNFVGMIALDALKDLMVH 121

QY	123	DAIDQLN	PAY	132
Db	122	DTIVNLQ	GVY	131

RESULT 4
 S22340
 seeligeriolysin - *Listeria seeligeri*
 C,Species: *Listeria seeligeri*
 C,Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C,Accession: S22340
 R,Haas, A.; Dumbeky, M.; Kreft, J.
 Biochim. Biophys. Acta 1130: 81-84, 1992
 A,Title: *Listeria*olysin gene: complete sequence of *ilo* from *Listeria ivanovi* and of *lsc*
 A,Reference number: S22340; PMID:92182016; PMID:1543752

A:Accession: S22340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1530 <HAA>
A:Cross-references: UNIPROT:P31830, EMBL:X60462, NID:g44144, PTDN:g44145
A:Note: the authors translated the codon GCC for residue 287 as Pro
C:Superfamily: dipeptide transport protein

Query Match	13.2%	Score 87.5;	DB 2;	Length 530;
Best Local Similarity	24.3%	Pred. No. 1;		
Matches 33, Conservative	23;	Mismatches 37;	Indels 43;	Gaps 7.

Qy	13	RDKGQTLVY--NPRGQNP	-----NGRASPQGA	-----VALLERK	48
		:: :	:: :		
Db	94	KDGEYIVAEKKKKGINQNNADISVINNI	SSLSTPGALYKANREL	VENQPNVLV	KRDSL 153

```

Qy 49 TWSISQPSNRKNYKQVKINPTACTANGSCDPSTR--QRY-----ADVFSEFQ 98
      ||| | :| :| ||| | :| | | :| :|
Db 154 TLSVDLPGMTKDKNKIFVK--NPTSNVNNAVNTLYERMNDKYSKAYPINAKIDYS--- 208

```

```
QY      99 YSTDEERAFVTELAA 114  
          :| | : :| |  
Db      209 ----DEMAYSESQLIA 220
```

RESULT 5
T00646
hymn of the

hypothetical protein F316_9 - *Arabidopsis thaliana*
CSpecies: *Arabidopsis thaliana* (mouse-ear cress)
CDate: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
CAccession: T00646
R.Federlepiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,
I.; Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologidis, A.; Davis, R.W.
Submitted to the EMBL Data Library, February 1998
A.Reference number: Z14197
A.Accession: T00646
A.Status: translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-540 <FED>
A.Cross-references: UNIPROT:O48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g28
C.Genetics:
A.Gene: ATSP:F316.9
A.Map position: 1
A.Introns: 14/3; 428/3; 448/2; 483/3; 502/3
C.Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binding

Query Match	12.9%	Score 85.5	DB 2	Length 540
Best Local Similarity	26.1%	Pred. No. 1.6		
Matches 30	Conservative 15	Mismatches 55	Indels 15	Gaps 3

QY 11 IGRGKQT/LVLPNG---VNPTNGVASLSQGAVPALKEKRTVSVSQPSPRRNKK-YKTQV 66
 : :: | : : ||| : | : : : :
D8 255 VKKEKKPNLIKNDGNVRINPTRGSLAKPNQVGKPETNKTYTSRKDPPSKEMKNMKATK 314

```

QY      67  KIQNPACTANGSDPSVRKQKVADYTFSPQYSTDERRAFVRIETALLASPLL 121
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      315  KPAPMKSQPGFATPRVYKPAPTKISLSTSHSLKKEK-----VSPLL 358

```

RESULT 6
S24231

RESULT 6
S24231
Listeriolysin precursor - Listeria monocytogenes (strain 12067)
A:Species: Listeria monocytogenes
A:Vaiety: strain 12067
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S24231
R:Ramuassen, O. F.; Beck, T.; Olsen, J.E.; Dons, L.; Rossen, L.
Infect. Immun. 59, 3945-3951, 1991
A:Title: Listeria monocytogenes isolates can be classified into two major types according
A:Reference number: S24230; MUID:92040062; PMID:1937753
A:Accession: S24231
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A;Residues: 1-529 <RAS>
A;Cross-references: UNIPROT:P13128; EMBL:X60035; NID:G44110; PID:CAA42639.1; PID:G44112
A;Experimental source: strain 12067, serotype 4b
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C;Genetics:
A;Gene: 118A
C;Superfamily: dipeptide transport protein
C;Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-529/Product: listeriolysin #status predicted <Mat>

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPTNGVASLSQAGA-----VPALEKRV 48
DB 93 KQGENETIVEKKKKKSIQNQNNADIQVNNALISLTYPGALVKANSELVENQDVLVPRGRDSL 152
QY 49 TVSVSQPSHRNRKRYKQVQIKQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
DB 153 TISIDPGMTNDNKTIKVR--NATKSNVNNAVNTLVERNNEKKAQAYPRVS---AKIDYD 207

QY 103 EERAFVETELAA 114
DB 208 DEMAYSESQLIA 219

RESULT 7
A;Residues: 1-529 <MEN>
A;Cross-references: UNIPROT:P13128; GB:M24199; NID:G149652; PIDN:AAA03018.1; PID:G149653
A;Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R;Domain, E.; Chakraborty, T.
Nucleic Acid Res. 17, 6406, 1989
A;Title: Nucleotide sequence of the listeriolysin gene from a *Listeria monocytogenes* ser
A;Reference number: S05306; MUID:8936684; PMID:2505236
A;Accession: S05306
A;Molecule type: DNA
A;Residues: 1-529 <DOM>
A;Cross-references: EMBL:X15127; NID:G44106; PIDN:CAA33223.1; PID:G44107
A;Experimental source: strain EGD
A;Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R;Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3227, 1987
A;Title: Identification of the structural gene encoding the SH-activated hemolysin of *L*
A;Reference number: A47606; MUID:88057627; PMID:2824384
A;Accession: A47606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <ME2>
A;Cross-references: GB:M29171
R;Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A;Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A;Reference number: S12400; MUID:91311627; PMID:1965218
A;Accession: S12400
A;Molecule type: DNA
A;Residues: 483-493 <MTC>
A;Experimental source: strain LO28, serotype 1/2c
C;Genetics:
A;Gene: hlyA, 118A

C;Superfamily: dipeptide transport protein
C;Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-529/Product: listeriolysin O #status predicted <Mat>

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPTNGVASLSQAGA-----VPALEKRV 48
DB 93 KQGENETIVEKKKKKSIQNQNNADIQVNNALISLTYPGALVKANSELVENQDVLVPRGRDSL 152
QY 49 TVSVSQPSHRNRKRYKQVQIKQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
DB 153 TISIDPGMTNDNKTIKVR--NATKSNVNNAVNTLVERNNEKKAQAYPRVS---AKIDYD 207

QY 103 EERAFVETELAA 114
DB 208 DEMAYSESQLIA 219

RESULT 8
A;Residues: 1-529 <GLA>
A;Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:G16409567; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: hly
C;Superfamily: dipeptide transport protein

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPTNGVASLSQAGA-----VPALEKRV 48
DB 93 KQGENETIVEKKKKKSIQNQNNADIQVNNALISLTYPGALVKANSELVENQDVLVPRGRDSL 152
QY 49 TVSVSQPSHRNRKRYKQVQIKQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
DB 153 TISIDPGMTNDNKTIKVR--NATKSNVNNAVNTLVERNNEKKAQAYPRVS---AKIDYD 207

QY 103 EERAFVETELAA 114
DB 208 DEMAYSESQLIA 219

RESULT 9
S57537
MKII protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein N2302; protein YNL085w
C;Species: *Saccharomyces cerevisiae*
C;Date: 10-Oct-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57537; S50279; S63024; S63017; S65096
R;Solier-Mira, A.; Saitz, U.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57533

A:Accession: S57537
A:Molecule type: DNA
A:Residues: 1-830 <SOL>
A:Cross-references: UNIPROT:P40850, EMBL:X89016; NID:9887621; PID:9887626
R:Vermt, M.; Widner, W.R.; Dimman, J.D.; Wickner, R.B.
Yeast 10, 1477-1479, 1994
A:Title: Sequence of MKT1, needed for propagation of M(2) satellite dsRNA of the L-A virus
A:Reference number: S50279; MUID:95176705; PMID:7532890
A:Accession: S50279
A:Molecule type: DNA
A:Residues: 1-29, 'G', 31-808, 'TAKTCUNYH' <VER>
A:Cross-references: EMBL:U09129; NID:9520475; PIDN:AA649470.1; PID:9520476
R:Solier-Mita, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
Submitted to the Protein Sequence Database, April 1996
A:Reference number: S63018
A:Accession: S63024
A:Molecule type: DNA
A:Residues: 1-830 <SOM>
A:Cross-references: EMBL:Z71361; NID:91301982; PID:91301983; MIPS:YNL085W
A:Experimental source: Strain S288C
R:Poehlmann, R.; Philippse, P.
Submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S63017
A:Molecule type: DNA
A:Residues: 569-830 <POE>
A:Cross-references: EMBL:Z71361; MIPS:YNL085W
A:Experimental source: Strain S288C
R:Solier-Mita, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
Yeast 12, 485-491, 1996
A:Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
A:Reference number: S65092; MUID:96310628; PMID:8740422
A:Accession: S65096
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-830 <SOF>
A:Cross-references: EMBL:X89016; NID:9887621; PIDN:CAA61425.1; PID:9887626
C:Genetic8:
A:Gene: SGD:MKT1
A:Cross-references: SGD:S0005029; MIPS:YNL085W
A:Map position: 14L
A:Superfamily: Saccharomyces cerevisiae MKT1 protein
C:Keywords: transmembrane protein
F:615-631/Domain: transmembrane #status predicted <TM>

Query Match 12.2%; Score 81; DB 2; Length 830;
Best Local Similarity 25.7%; Pred. No. 7.5;
Matches 26; Conservative 20; Mismatches 49; Gaps 6; Gaps 3;

Oy 5 TTTTGGTCGRDQKQTLVLPNGVNPFGVASSQAGAVALEKRVTSVSGPSRRKRYKV 64
Db 301 STTQGN--DKENIQNYQRGISALRYKVPYKDRQKVELFYQELVTSSEDSKNNKQK- 356

Oy 65 QVKIQNPACTANGSCDPSVTRQKYADVTFSTFYQSTDEER 105
Db 357 KSNLSSPS--SASSSASPATVTVTKNASSEKLTYEKSTVEVR 395

RESULT 10
KGBYH1
CYC1/CY3 transcription activator - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein I9672.1; protein YLR566w; regulatory protein CYP1; regulatory protein CYP1;
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1991 #sequence revision 23-Feb-1996 #text_change 12-Nov-1999
A:Accession: S59400; A31312; S15447; S05804; S15446
R:Johnson, D.
Submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9672.
A:Reference number: S59386
A:Accession: S59400
A:Molecule type: DNA
A:Residues: 1-1502 <JOH>
A:Cross-references: EMBL:U20865; NID:9662330; PIDN:AA867387.1; PID:9662331; GSPDB:GN00001

```

A|Experimental source: strain S288C (AB972).
R|Peifer, K.; Kim, K.S.; Kogan, S.; Quarente, L.
Cell 56, 291-301, 1989
A>Title: Functional dissection and sequence of yeast HAP1 activator.
I|Reference number: A1312; MUID:89106221; PMID:2643482
A|Molecule type: DNA
A|Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'W', 509-586, 'K', 588-882, 'N', 884-955
A|Cross-references: EMBL:J03152; NID:g171645; PID:AA34662.1; PID:g171646
R|Crausot, F.; Verdier, J.; Galsne, M.; Slonimski, P.P.
J.Mol. Biol. 204, 263-276, 1988
A>Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall c
A|Reference number: S15447; MUID:89125585; PMID:2851658
A|Accession: S15447
A|Molecule type: RNA
A|Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYADPIWE' <CRE1>
A|Cross-references: EMBL:X13793
A>Note: the sequence is from mutant CYP1-18
C|Genetics:
A|Gene: SGD:HAP1; CYP1; MIPS:YLR256w
A|Cross-references: SGD:S0004246; MIPS:YLR256w
A|Map position: 12R
C|Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology
C|Keywords: DNA binding; heme binding; hestatus predicted <DNA>
F:1-148/Domain: DNA binding #status predicted <DNA>
F:15-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F:64-84/Region: zinc finger CCCC motif
F:177-189/Region: glutamine-rich
F:245-445/Domain: heme binding #status predicted <HEM>
F:299-304,323-328,337-352,373-378,389-394,415-420/Region: 6-residue repeats
F:1368-1481/Domain: activation element #status predicted <ACT>
F:1388-1481/Region: acidic

Query Match          12.1%; Score 80.5; DB 1; Length 1502;
Best Local Similarity 20.6%; Pred. No. 17;
Matches    35; Conservative   30; Mismatches     42; Indels    63; Gaps      7;

QY 23 PRGVV--PTNGVASI-----SQAGVPALKERVTVSVS 53
      |||||:::|||:-:|||||:|||||:|||||:|||||:
Db 1278 PRGSPKNSGLSSVQLPLISSNMNLGCTIPYPSLTNITSQMHLPSLDRTTMOIN 1337

QY 54 QPSNR-KNYKVQVKIONP-----TACTANGSCP 82
      |||:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:
Db 1338 LPDSRDPAFDMSIKOMPTMTSAFMNANTTIPSTLGNMNMAGATNDTSANGSALS 1397

QY 83 SVTRQKADV-TFSFTQYSTD-EERAFVTELLALASP-LIIDAIQDN 129
      ::|:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:
Db 1398 TLTSPOGSLANSATQYKPDLDEPLMNQSNFNGLMNPSSLVEVGGIN 1447

RESULT 11
S22341
Ivanoliyain precureor - Listeria ivanovi
C|Species: Listeria ivanovi
C|Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #ext_change 09-Jul-2004
A|Accession: S22341; S36683
R:Haas, A.; Dumbsky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A>Title: Listeriolysin genes: complete sequence of ilo from Listeria ivanovi and of lso
A|Reference number: S22340; MUID:92182018; PMID:1543752
A|Accession: S22341
A|Molecule type: DNA
A|Residues: 1-528 <HAS>
A|Cross-references: UNIPROT:P31831; EMBL:X60461
A>Note: the authors translated the codon ACA for residue 331 as Val
R:Kreft, J.
submitted to the EMBL Data Library, July 1991
A|Reference number: S36683
A|Accession: S36683
A|Molecule type: DNA
A|Residues: 1-319, 'T', 321-528 <KRE>
A|Cross-references: EMBL:X60461
C|Genetics:

```

A:Gene: 110
C:Superfamily: dipeptide transpore protein
P:1-24/Domain: signal sequence <Sig-
F:25-528/Product: 1vanolysin #status predicted <Mtr>

Query Match 11.7%; Score 77.5; DB 2; Length 528;
Best Local Similarity 21.2%; Pred. No. 9.8;
Matches 28; Conservative 25; Mismatches 44; Indels 35; Gaps 5;

QY 13 RGGKQNLV-----NPRGVNPNNGVSLSQAG-----VPALEKRY 48
DB 92 KGGNQITVEKKKKKSIQNNADIQVINSLSLTPALVYKANSLEVENQDVLPRKDSV 151
QY 49 TVSVSQPSRRKRYKQVQKIQNPTACTANGSCDPSVTR-----QKXADVTFSFTQSTD 102
DB 152 TISIDLP--GMVNHDEIVQVQNTKSNINDGVTLVDRMNNKSEEPNLS---AKIDVD 206
QY 103 EERAFVETELAA 114
DB 207 QEMAYSESOLVA 218

RESULT 12

TJ1660
hypothetical protein COS41.6 - sea equit (Clona intestinalis)
C:Species: Clona intestinalis
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: TJ1660
R:Bird, A.P., Clark, V., Jones, S.J., Leitgeb, S., Dobson, R., Tweedie, S.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z21049
A/Accession: TJ1660
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-432 <BIR>
A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CAB0605
C:Genetics:
A:introns: 180/2; 212/1; 229/3

Query Match 11.6%; Score 77; DB 2; Length 432;
Best Local Similarity 27.4%; Pred. No. 8.7;
Matches 31; Conservative 17; Mismatches 47; Indels 18; Gaps 6;
QY 4 ETVTLLNIGRDGKQTLVLPNGVNPNGVSLSQAGVPALEKRYTVSVSQPSRRKRYK 63
DB 242 DSSSEGVTKDGGNLAENP---TPSNARELOESVASEVLETTVYKSAIQ--EQDSAR 237
QY 64 VQVKIQNPAC--TANGSC-----DPSVTRQRYAD---VTFSTQYSTDE 103
DB 298 KE-NPQNAACPFRNGNCVSTNSNKTPNDSKIEIVNSDNTTDEDTQIDITNE 349

RESULT 13
C98221
hypothetical protein AGR_L_1428 [imported] - Agrobacterium tumefaciens (strain C58, Cerc
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: C98221
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman,
A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2333-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MWID:21608551; PMID:11743194
A/Accession: C98221
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <NUR>
A:Cross-references: UNIPROT:Q8U8F3; GB:AE007870; PIDN:AKG9293.1; PID:G15159127; GSPDB:G
C:Genetics:
A:Gene: AGR_L_1428
A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;
Best Local Similarity 24.6%; Pred. No. 2.5;
Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;
QY 11 IGRDGKQTLVLPNGVNPNGVSLSQAGV-----PALERVTVSQPSRRN 59
DB 3 ISKDGKQTESADPHWLEWVTGTISTLLVAMGMAVYDIYRSPPEARFEIAVTVGEGQT 62
QY 60 KMYKQVQKIQNPACTA-----NGSCDPSVTRQRYADVTFSF--TQYSTDEERAFVTE 111
DB 63 GQYRVKFAIHNLSMTTAAQVNVRGDLEQNGASPEBNADVTFDYVASSKONGTLFFRSD 120

RESULT 14
AE3065
conserved hypothetical protein Atu4139 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AE3065
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woe, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavin, T.; Levy, R.; Li, M.; Mclell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MWID:21608550; PMID:11743193
A/Accession: AE3065
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <NUR>
A:Cross-references: UNIPROT:Q8U8F3; GB:AE008689; PIDN:ALL44939.1; PID:G17742593; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4139
A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;
Best Local Similarity 24.6%; Pred. No. 2.5;
Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;
QY 11 IGRDGKQTLVLPNGVNPNGVSLSQAGV-----PALERVTVSQPSRRN 59
DB 3 ISKDGKQTESADPHWLEWVTGTISTLLVAMGMAVYDIYRSPPEARFEIAVTVGEGQT 62
QY 60 KMYKQVQKIQNPACTA-----NGSCDPSVTRQRYADVTFSF--TQYSTDEERAFVTE 111
DB 63 GQYRVKFAIHNLSMTTAAQVNVRGDLEQNGASPEBNADVTFDYVASSKONGTLFFRSD 120

RESULT 15
C64221
hypothetical 114K protein (Mgpa 3' region) - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C/Accession: C64221; J00092; S18702; S18703
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.J.
Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MWID:96026346; PMID:7569993
A/Accession: C64221
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1052 <TIGR>
A:Cross-references: UNIPROT:P22747; GB:U39696; GB:L43967; NID:G1045869; PID:G1045877; TIC
A:Experimental source: strain G-37
R:Linane, J.M.; Loebel, S.; Collier, A.M.; Barile, M.F.; Hu, P.C.
Gene 82, 259-267, 1989
A>Title: Nucleotide sequence of the Mgpa (mgp) operon of Mycoplasma genitalium and compa
A:Reference number: J00090; MWID:90060815; PMID:2583522
A/Accession: J00092
A:Molecule type: DNA

Query Match 11.5%; Score 76.5; DB 2; Length 136;
Best Local Similarity 24.6%; Pred. No. 2.5;
Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;
QY 11 IGRDGKQTLVLPNGVNPNGVSLSQAGV-----PALERVTVSQPSRRN 59
DB 3 ISKDGKQTESADPHWLEWVTGTISTLLVAMGMAVYDIYRSPPEARFEIAVTVGEGQT 62
QY 60 KMYKQVQKIQNPACTA-----NGSCDPSVTRQRYADVTFSF--TQYSTDEERAFVTE 111
DB 63 GQYRVKFAIHNLSMTTAAQVNVRGDLEQNGASPEBNADVTFDYVASSKONGTLFFRSD 120

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-8
Perfect score: 664
Sequence: 1 ARLFTVLTGNIGRDGKQTLV.....ALLASPLILDAIDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.2	132	1	COAT BPQBE
2	652	98.2	132	1	AAM3J126
3	652	98.2	132	2	AA1663
4	652	98.2	132	2	AA1663
5	651	84.5	133	2	Q9T0R9
6	561	84.5	132	2	Q9T0S0
7	541	81.5	133	2	Q9T0S0
8	541	81.5	132	1	COAT BPSP
9	526.5	79.3	132	1	COAT BPSP
10	526.5	79.3	131	1	VAL BPSP
11	493.5	74.3	132	2	Q9T0R8
12	493.5	74.3	130	2	Q64310
13	116	17.5	131	1	COAT BPSP
14	96.5	14.5	131	1	Q8VDC2
15	87.5	13.2	530	1	TACY L1SSB
16	87.5	13.2	530	1	AA897361
17	85.5	12.9	540	2	Q48683
18	82	12.3	512	2	Q6HGA7
19	81.5	12.3	529	1	TACY L1SMP
20	81.5	12.3	529	1	TACY L1SMP
21	81.5	12.3	529	2	Q9L5B9
22	81.5	12.3	529	2	Q6E8A2
23	81.5	12.3	529	2	Q6E8A2
24	81.5	12.3	529	2	Q6E8A2
25	81.5	12.3	529	2	Q6E8A2
26	81.5	12.3	529	2	Q6E8A2
27	81.5	12.3	529	2	Q6E8A2
28	81.5	12.3	529	2	Q6E8A2
29	81.5	12.3	529	2	Q6E8A2
30	81.5	12.3	529	2	Q6E8A2
31	81.5	12.3	529	2	Q6E8A2

32	81.5	12.3	529	2	AAT03000	AAT03000 listeria
33	81	12.2	325	2	Q73R79	Q73R79 treponema d
34	81	12.2	325	2	AAS10709	AAS10709 treponema
35	81	12.2	830	1	MKT1 YEAST	P40850 saccharomyc
36	81	12.2	830	2	Q8TF87	Q8TF87 saccharomyc
37	81	12.2	830	2	Q8TF89	Q8TF89 saccharomyc
38	81	12.2	830	2	Q8TF85	Q8TF85 saccharomyc
39	81	12.2	830	2	Q8TF85	Q8TF85 saccharomyc
40	81	12.2	830	2	Q8TF85	Q8TF85 saccharomyc
41	81	12.2	830	2	Q8TF85	Q8TF85 saccharomyc
42	81	12.2	1624	2	Q9V3K8	Q9V3K8 drosophila
43	81	12.2	1637	2	Q9V3K8	Q9V3K8 drosophila
44	80.5	12.1	1502	1	CYPI YEAST	P12351 saccharomyc
45	79.5	12.0	608	2	Q84H79	Q84H79 rhodococcus

ALIGNMENTS

RESULT 1
COAT_BPQBE STANDARD; PRT; 132 AA.
ID COAT_BPQBE
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviriviruses.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clelens I., Dreilima D., Dislers A., Baumanis V.,
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RL assembled in Escherichia coli.",
Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarot C., Sastre P.A., Billeter M.A.,
RT "Determination of the first half of the coat protein cistron of
RL bacteriophage Q-beta as an application of a mapping procedure for RNA
fragments.",
J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.,
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
and 60.",
J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maite T., Konigsberg W.,
RT "The amino acid sequence of the Q-beta coat protein.",
J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Valiegard K., Lilljas L.,
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.",
Structure 4:543-554(1996).
RL Structure 4:543-554(1996).
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CC EMBL; M99039; AAA16662.1; -
 CC EMBL; V00643; CAA33992.1; -
 DR PIR; A92240; VCBPOB.
 DR PDB; 1QBE; X-ray; A/B/C=1-132.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
 FT INIT MET 0 0 N -> D (in Ref. 4).
 FT CONFLICT 22 22 Missing (in Ref. 4).
 FT CONFLICT 56 56
 FT STRAND 6 9
 FT TURN 13 14
 FT TURN 18 27
 FT TURN 28 31
 FT STRAND 32 36
 FT STRAND 42 44
 FT HELIX 47 53
 FT STRAND 56 56
 FT TURN 57 58
 FT STRAND 59 59
 FT STRAND 62 74
 FT STRAND 83 96
 FT TURN 98 99
 FT HELIX 102 117
 FT HELIX 119 126
 FT TURN 127 127
 SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA572E CRC64;

Query Match 98.2%; Score 652; DB 1; Length 132;
 Best Local Similarity 97.7%; Pred. No. 1.3e-55;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQYADVTFSFTQYSTDEERAFVTELAALIASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQYADVTFSFTQYSTDEERAFVTELAALIASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 2
 AAM33126 PRELIMINARY; PRT; 133 AA.
 ID AAM33126
 AC AAM33126.
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OS viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviridae; Alloviridae subgroup III.
 OC NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Bacher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes."
 RL BMC Evol. Biol. 3:24-24(2003).
 DR EMBL; AY099114; AAM33126.1; -
 KW Coat protein.
 SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.2%; Score 652; DB 2; Length 133;
 Best Local Similarity 97.7%; Pred. No. 1.4e-55;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 DB 2 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 61
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQYADVTFSFTQYSTDEERAFVTELAALIASPL 120
 DB 62 NYKVQVKIQNPACTANGSCDPSVTRQYADVTFSFTQYSTDEERAFVTELAALIASPL 121
 QY 121 LIDAIDQLNPAY 132
 DB 122 LIDAIDQLNPAY 133

RESULT 3
 Q8LTEL1 PRELIMINARY; PRT; 329 AA.
 ID Q8LTEL1
 AC Q8LTEL1
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE A1 read-through protein (A1 protein).
 OS Bacteriophage Q-beta.
 OS viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviridae;
 OC NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Bacher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes."
 RL BMC Evol. Biol. 3:24-24(2003).
 SQ SEQUENCE FROM N.A.
 RP MEDLINE=94109687; PubMed=7506687;
 RX Kozlovskaya T.M., Clemons I., Drellina D., Dieters A., Bauman V.,
 RA Ose V., Pumpens P.;
 RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
 assembled in Escherichia coli."
 RL Gene 137:133-137(1993).
 DR EMBL; AY099114; AAM33127.1; -
 DR EMBL; M99039; AAA16663.1; -
 DR HSP; P03615; IQBE.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1_coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.2%; Score 652; DB 2; Length 329;
 Best Local Similarity 97.7%; Pred. No. 3.9e-55;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 DB 2 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 61
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQYADVTFSFTQYSTDEERAFVTELAALIASPL 120
 DB 62 NYKVQVKIQNPACTANGSCDPSVTRQYADVTFSFTQYSTDEERAFVTELAALIASPL 121
 QY 121 LIDAIDQLNPAY 132
 DB 122 LIDAIDQLNPAY 133

RESULT 4
 AAA16663 PRELIMINARY; PRT; 329 AA.
 ID AAA16663
 AC AAA16663
 DT 02-MAR-2004 (Tremblrel. 27, Created)

DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DS A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviriviruses.
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A..
RX MEDLINE=94103687; PubMed=7506687;
RA Kozlovskaya T.M., Clemons I., Drellina D., Dislers A., Baumanns V.,
RA Ose V., Pumpens P.,
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.",
RT Gene 137:133-137(1993).
DR EMBL, M99039: AAA16663.1; --
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match	98.2%	Score	652	DB 2	Length	329
Best Local Similarity	97.7%	Pred.	No. 3.9e-55			
Matches 129	Conservative	2	Mismatches	1	Indels	0
					Gaps	0

Qy	1	ARLEVTJLGNIGRDO	KQTLVYNPREVNP	PTNGVSAJSQGA	VPALKEKRTVSV	QSSRRK	60
	:	:	:	:	:	:	
Db	2	AKLEVTJLGNIGK	QKQTLVYNPREVNP	PTNGVSAJSQGA	VPALKEKRTVSV	QSSRRK	61
Qy	61	MYKQVKNQNTACTA	NGSCDPSVTRQKAD	VTSEFTQYSTDERA	FAFRTTEAALLA	SP	120
Db	62	MYKQVKNQNTACTA	NGSCDPSVTRQKAD	VTSEFTQYSTDERA	FAFRTTEAALLA	SP	121
Qy	121	LIDAIIDQINPAY					132
Db	122	LIDAIIDQINPAY					133

RESULT 5	
Q9TOR9	
ID	O9TOR9 PRELIMINARY; PRT; 133 AA.
AC	O9TOR9;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Major coat protein.
OS	Enterobacteriophage MX1.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC	Allolevivirus.
OX	NCBI_TaxID=75723;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=85239761; PubMed=7723040;
RA	Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT	"Secondary structure model for the last two domains of single-stranded
RT	RNA phase Q beta.";
RL	J. Mol. Biol. 247:903-917(1995).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96190948; PubMed=8609616;
RA	Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT	"Secondary structure model for the first three domains of Q beta RNA.
RT	Control of A-protein synthesis.";
RL	J. Mol. Biol. 256:8-19(1996).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL, AF059242; AAC1469.1; -.
DR	HSCP, P03615; IQBE.
DR	GO; GO:0019028; C:viral capsid; IBA.
DR	GO; GO:0005198; F:structural molecule activity; IBA.
DR	InterPro; IPR002703; Lev1_coat.
DR	Pfam; PF01819; Lev1_coat; 1.
DR	Coat protein.
QO	SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;

Query Match Similarity	84.5%	Score 561	DB 2	Length 133
Best Local Similarity	81.8%	Pred. No. 1e-46		
Matches 108	Conservative 12	Mismatches 12	Indels 0	Gaps 0

Qy	1	ARLETVILGNIGRGCKOTLVLPFGVNPPTNGVASLSQAGVAPALEKEKVTWVSQPSNRK	60
	2	AKQDAILTSGIGKKGDVTLNLPNGVNPPTNGVALLSEAGVAPALEKEKVTISVQPSNRK	61
Qy	61	NYKQVKNIOPLPACTAGSCDPSVTRQKRYADYFESFYQSTDEERAAVFRVREILAAI,LA,SPL	120
	62	NYKQVAKIQNPLSTCLAGTCDPSVTRSAVADYFESFYQSTDEERAAVFRVREILKALLADPM	121
Qy	121	LIDAIDQLNPAY	132
	122	LIDAIDNLNPAY	133

RESULT 6	
064307	
ID	064307
AC	064307;
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	A1-protein.
OS	Enterobacteria phage MX1.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage, Leviviridae;
OC	Allolevivirus.
NCBI_TaxID=75723;	
NCBI_TaxID=75723;	

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RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF059242; AAC14700.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_cat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Levi_cat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
QO SEQUENCE 329 AA; 35880 MW; 372B1DD50DBE2F15 CRC64;

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[illegible]

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RESULT 7
O9T0S0      PRELIMINARY;      PRT;      133 AA.
AC 09T0S0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Coat protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus
NCBI_TaxID=74336;
RN
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
[2]
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
[3]
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coat protein.
KM
SQ SEQUENCE 133 AA; 14198 MW; 098722E3C6C3A255 CRC64;

Query Match      81.5%; Score 541; DB 2; Length 133;
Best Local Similarity 78.8%; Pred. No. 9e-45;
Matches 104; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 ARLEVTYLTGNIGDGKQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNK 60
DB 2 AKLQATTLTSGIKKGQVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALADPM 121
QY 121 LIDAIDQINPAY 132
DB 122 LVNAIDMINPAY 133

RESULT 8
O64303      PRELIMINARY;      PRT;      329 AA.
AC 064303;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=74336;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
[2]
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
[3]
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06251.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RNM_RNP_1; UNKNOWN 1.
DR SEQUENCE 329 AA; 35893 MW; 3E33CDB21EE625F4 CRC64;

Query Match      81.5%; Score 541; DB 2; Length 329;
Best Local Similarity 78.8%; Pred. No. 2.6e-44;
Matches 104; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 ARLEVTYLTGNIGDGKQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNK 60
DB 2 AKLQATTLTSGIKKGQVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALADPM 121
QY 121 LIDAIDQINPAY 132
DB 122 LVNAIDMINPAY 133

RESULT 9
COAT BPSP      STANDARD;      PRT;      132 AA.
ID COAT BPSP
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=12027;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3393930;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT Coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC
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CC
CC EMBL; X07489; CAA30374.1; -.
DR HSSP; P03615; IQBE.

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DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein; RNA-binding.
 SQ SEQUENCE 132 AA; 14129 MW; 50B1E6CC6AFOA254 CRC64;

Query Match 79.3%; Score 526.5; DB 1; Length 132;
 Best Local Similarity 77.3%; Pred. No. 2.3e-43;
 Matches 102; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLEVTYLGNIIGRDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSOPSRRNK 60
 DB 2 AKLNQVTLSTKIGNGQTLTLTPRGVNPPTNGVSLSGAGVPALEKRVTVSVAQPSRRNK 61
 QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 62 NFKVQKIQNPACTCTRD-ACDPSVTRSAFADVTLSFTYSTDERALLIRTELAALLADPL 120
 QY 121 LIDAIQDLPAY 132
 DB 121 IYDAIDNLNPAY 132

RESULT 10
 VAI_BPSP STANDARD; PRT; 331 AA.

AC P09677;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Reactthrough protein A1 [Contains: Coat protein].
 OS Bacteriophage SP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allolievirus.
 OX NCBI_Taxid=12027;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82829362; PubMed=3399390;
 RA Hirashina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
 RT "Analysis of the complete nucleotide sequence of the group IV RNA
 collapse SP".
 RL Nucleic Acids Res. 16:6205-6221(1988).
 CC -1- FUNCTION: Not yet known.
 CC -1- MISCELLANEOUS: The reactthrough protein A1 includes the coat
 protein sequence.

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EMBL; X07489; CAB37299.1; -.
 DR PIR; S01964; S01964.
 DR HSSP; P03615; IOBE.
 DR InterPro; IPR002703; Lev1_coat.

DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein.
 FT CHAIN 1 132
 FT CHAIN 1 331
 SQ SEQUENCE 331 AA; 36203 MW; 4A664284B52C6582 CRC64;

Query Match 79.3%; Score 526.5; DB 1; Length 331;
 Best Local Similarity 77.3%; Pred. No. 6.8e-43;
 Matches 102; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLEVTYLGNIIGRDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSOPSRRNK 60
 DB 2 AKLNQVTLSTKIGNGQTLTLTPRGVNPPTNGVSLSGAGVPALEKRVTVSVAQPSRRNK 61
 QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 121 IYDAIDNLNPAY 132

DB 62 NFKVQKIQNPACTCTRD-ACDPSVTRSAFADVTLSFTYSTDERALLIRTELAALLADPL 120
 QY 121 LIDAIQDLPAY 132
 DB 121 IYDAIDNLNPAY 132

RESULT 11
 O9TOR8 PRELIMINARY; PRT; 132 AA.

ID O9TOR8
 AC O9TOR8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allolievirus.
 OX NCBI_Taxid=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RT RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.

DR EMBL; AF059243; AAC14703.1; -.
 DR HSSP; P03615; IOBE.
 DR GO; GO:0019028; C: viral capsid; IBA.
 DR GO; GO:0005198; F: structural molecule activity; IBA.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein.
 SQ SEQUENCE 132 AA; 14143 MW; 6727093757F22EA CRC64;

Query Match 74.3%; Score 493.5; DB 2; Length 132;
 Best Local Similarity 74.2%; Pred. No. 3.8e-40;
 Matches 98; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

QY 1 ARLEVTYLGNIIGRDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSOPSRRNK 60
 DB 2 AKLNQVTLSTKIGNGQTLTLTPRGVNPPTNGVSLSGAGVPALEKRVTVSVAQPSRRNK 61
 QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 62 NYKVQKIQNPACTCTRD-ACDPSVTRSGSRDVTLSFTYSTDERALLIRTELAALLADPL 120
 QY 121 LIDAIQDLPAY 132
 DB 121 IYDAIDNLNPAY 132

RESULT 12
 O64310 PRELIMINARY; PRT; 330 AA.

ID O64310
 AC O64310;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE A1-protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC Allollevirus.
 OX NCBI_TaxID=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSSP; P03615; IOBE.
 DR GO; GO:0019028; C.viral capsid; IEA.
 DR GO; GO:0005198; F.structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR InterPro; PS00030; RRM_RNP_1; UNKNOWN 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 961B55F408334410 CRC64;

Query Match 74.3%; Score 493.5; DB 2; Length 330;
 Best Local Similarity 74.2%; Pred. No. 1.1e-39;
 Matches 98; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

QY 1 ARLETTVLNIGDQKQTLVLRGVNPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
 DB 2 AKNKVTLTIGAGNQTLTLTRGVNPTNGVASLSQAGAVPALERKVTYSVQPSNRK 61
 QY 61 NYKQVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPL 120
 DB 62 NYKQVQKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPL 120
 QY 121 LIDAIQQLNPAY 132
 DB 121 IVDAILDNLNPAY 132

RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1.";
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein; Direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B639E1E50FC612 CRC64;

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0024;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;

QY 17 QTLVLRGVNPT-----NGVASLSQAGAVPALERKVTYSVQPSNRKKNKQV 66
 DB 4 QNLVLDRKREPTDHTFVPDIDNVGEVSESGVIGSRFTLSRKTSNGR--YKSTL 61
 QY 67 KIQNP--ACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETLAALLASPLLI- 122
 DB 62 KLVPEVQGTGVTGIVTPPVVTRTSYTVDPDYARSTTKERNNFVGMIDLAKADMLVH 121
 QY 123 DAIDQQLNPAY 132
 DB 122 DRIVLQGVY 131

RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2
 AC Q8VDC2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Trmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BALB/c; TISSUE=Liver;
 RC MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darai E., Kiss C., Koest-Alimova M., Klein G., Dumanek J.P.,
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3.";
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL; AJ428064; CAD20986.1; -.
 DR MGD; MGI:2446841; Trmem7.
 DR GO; GO:0016021; C.integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0E69F2A4D CRC64;

Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.88;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;

QY 5 TVTLSNIGRDGKQTLV-----LNRGVNPTNG--VASLSQAGAVP-----ALEK 46
 DB 195 TATCSNISSSQPSKQWMPQASKANQASNPTRKNDPKVCTSKPAPPLSPSTLSKAREP 254
 QY 47 RLVVSVSQPSRKRNKQV-----KIQNP-----ACTANGSCDPSVTRQ----- 87
 DB 255 KVLVTCNISSSSSSKVQMPQASKVNPQTSNPTKNDPKVCTSKPSTPRLTIQQLSVV 314
 QY 88 -----KYADVTFSTQYSTDERAFVRETLAALLASPLLI 122
 DB 315 SPPAPAPTCVQWPSPTPIDSGRAADVAKENRSTKPK-----ALLSPLVY 361

RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligerolysin precursor (Thiol-activated cytolysin).
 GN Name=Iso;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

```

OK NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLC;
RX MEDLINE=92182018; PubMed=1543752;
RA Haas A.; Dumbeky M., Kreft J.;
RT "Listeriolysin genes: complete sequence of ilo from Listeria ivanovi
and of iso from Listeria seeligeri."
RL Biochim. Biophys. Acta 1130:81-84(1992).
CC -! FUNCTION: Sulphydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
Cholesterol is the receptor for the binding of these toxins to
eukaryotic cell membranes.
CC -! SIMILARITY: Belongs to the thiol-activated cytolysin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X60462; CAA42996.1; -.
CC PIR; S22340; S22340.
CC DR HSSP; P19995; 1PFO.
CC DR InterPro; IPR001869; Thiol_cytolysin.
CC DR Pfam; PF01289; Thiol_cytolysin; 1.
CC DR PRINTS; PR01400; TACTOLYSIN.
CC DR ProDom; PD007062; Thiol_cytolysin; 1.
CC DR PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
CC KW Cytolysis; Hemolysis; Lipid-binding; Signal; Toxin.
CC FT SIGNAL 1 25
CC FT CHAIN 26 530 Seeligerolysin.
CC FT SITE 485 485 Binding to cholesterol (By similarity).
CC SQ SEQUENCE 530 AA; 59181 MW; 416F7A4DD2029866 CRC64;

```

```

Query Match 13.2%; Score 87.5; DB 1; Length 530;
Best Local Similarity 24.3%; Pred. No. 7.6;
Matches 33; Conservative 23; Mismatches 37; Indels 43; Gaps 7;

```

```

QY 13 RDGKQTLV--NRGVNPT-----NGVASLSQAG-----VPALEKRV 48
   :||: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 94 KDGSEYIVVEKKKKGINNNADISVINAIISLTYPGALVKNRELVENQPNVL PVKRDSTL 153
   ||||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 49 TVSVSQSPSNRRKKYKQVKNQNTACTANGSCDPSYTR--QKY-----ADVFSTFQ 98
   ||||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 154 TUSVDLPGMTKKDKNKL FVK--NPTKSNVNNVAVTLVERMNDKYSKAYPNINAKIDYS--- 208
   ||||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 99 YSTDEERAFVETELAA 114
   :||: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 209 ----DEMAYSESQLIA 220

```

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Search completed: January 4, 2005, 09:16:16
Job time : 37.2676 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-7

Perfect score: 653
Sequence: 1 AKETVTLGKIGKDGKQTLV.....AALASPILLDAIDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	132	5	ABG94317
2	663	100.0	132	5	ABG80629
3	663	100.0	132	6	ABR56453
4	663	100.0	132	6	ABU09690
5	663	100.0	132	6	ABR44556
6	663	100.0	132	7	ADJ24131
7	663	100.0	132	7	ADJ82057
8	663	100.0	132	7	ADK17145
9	663	100.0	132	8	ADJ36314
10	663	100.0	132	8	ADJ67160
11	663	100.0	132	8	ADK52194
12	663	100.0	132	8	ABG94316
13	663	100.0	132	5	ABG94320
14	663	100.0	132	5	ABG80632
15	663	100.0	132	5	ABG80632
16	663	100.0	132	6	ABR56455
17	663	100.0	132	6	ABR56452
18	663	100.0	132	6	ABU09689
19	663	100.0	132	6	ABU09693
20	663	100.0	132	6	ABR44555
21	663	100.0	132	6	ABR44558
22	663	100.0	132	7	ADJ24130
23	663	100.0	132	7	ADJ24133
24	663	100.0	132	7	ADJ82059
25	663	100.0	132	7	ADJ82056

26	655	98.8	132	7	ADK17144	ADK17144
27	655	98.8	132	7	ADK17147	ADK17147
28	655	98.8	132	8	ADJ36316	ADJ36316
29	655	98.8	132	8	ADJ36313	ADJ36313
30	655	98.8	132	8	ADJ67159	ADJ67159
31	655	98.8	132	8	ADJ67162	ADJ67162
32	655	98.8	132	8	ADK52196	ADK52196
33	655	98.8	132	8	ADK52193	ADK52193
34	652	98.3	132	5	ABG94233	ABG94233
35	652	98.3	132	5	ABG94318	ABG94318
36	652	98.3	132	5	ABG94319	ABG94319
37	652	98.3	132	5	ABG80630	ABG80630
38	652	98.3	132	5	ABG80631	ABG80631
39	652	98.3	132	5	ABG80545	ABG80545
40	652	98.3	132	6	ABR56454	ABR56454
41	652	98.3	132	6	ABR56456	ABR56456
42	652	98.3	132	6	ABR56439	ABR56439
43	652	98.3	132	6	ABU09686	ABU09686
44	652	98.3	132	6	ABU09692	ABU09692
45	652	98.3	132	6	ABU09691	ABU09691

ALIGNMENTS

RESULT 1
ID ABG94317 standard; protein; 132 AA.
XX
AC ABG94317;
XX
DT 29-AUG-2003 (revised)
DT 10-DEC-2002 (first entry)
XX
DE pOB243 protein.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
OS unidentified bacteriophage.
XX
FN W0200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002MO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Plossek C;
XX
DR WPI; 2002-627351/67.
XX
PS Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX
PS Claim 18; Page 144; 441pp; English.
XX
This invention relates to a novel ordered and repetitive antigen array
XX used in the production of vaccines for infectious diseases. The invention
XX also discloses a composition comprising a non-natural molecular scaffold
XX comprising a core particle selected from a core particle of a non-natural
XX origin and a core particle of natural origin and an organiser comprising
XX at least one first attachment site, where the organiser is connected to
XX the core particle by at least one covalent bond. Also disclosed is an
XX antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTVLGKIGKQKQKOTLVNPRGVNPTNGVASHQAGVPALEKRYTVSVSOPSRNRK 60

Db 1 AKLEVTVLGKIGKQKQKOTLVNPRGVNPTNGVASHQAGVPALEKRYTVSVSOPSRNRK 60

Qy 61 NYKQVQKIQNPTACTANGSCDPSVTRQKADVTFTSYSDTERAFVETELAAALLSPL 120

Db 61 NYKQVQKIQNPTACTANGSCDPSVTRQKADVTFTSYSDTERAFVETELAAALLSPL 120

Qy 121 LIDAIDQNPAY 132

Db 121 LIDAIDQNPAY 132

RESULT 2

ABG80629

ID ABG80629 standard; protein; 132 AA.

XX ABG80629;

XX 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-243.

KM Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IGF-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious diseases; factor Xa;
 KM enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.

OS Synthetic.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-1B000168.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326988P.

XX 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LBOE/) LBOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.

XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;
 PI Renner W, Bachmann M, Tissot A, Seibel P, Ploesek C;
 XX WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

XX Example 18; Page 144; 418pp; English.

CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organism comprising at least one first attachment
 CC site, where the organism is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGF-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy, immunoblastic lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTVLGKIGKQKQKOTLVNPRGVNPTNGVASHQAGVPALEKRYTVSVSOPSRNRK 60

Db 1 AKLEVTVLGKIGKQKQKOTLVNPRGVNPTNGVASHQAGVPALEKRYTVSVSOPSRNRK 60

Qy 61 NYKQVQKIQNPTACTANGSCDPSVTRQKADVTFTSYSDTERAFVETELAAALLSPL 120

Db 61 NYKQVQKIQNPTACTANGSCDPSVTRQKADVTFTSYSDTERAFVETELAAALLSPL 120

Qy 121 LIDAIDQNPAY 132

Db 121 LIDAIDQNPAY 132

RESULT 3

ABR56453

ID ABR56453 standard; protein; 132 AA.

XX ABR56453;
AC 28-JUL-2003 (first entry)
XX Bacteriophage Q-beta coat protein mutant SEQ ID NO:24.
XX
XX Antigen presenting cell; ADC; immune response; virus like particle; VLP;
XX cytosolic; virucide; antibacterial; antiparasitic; fungicide;
XX antiallergic; immunosuppressive; antiaddictive; antitumorigenic;
XX antihypertensive; antidiabetic; neuroprotective; nootropic; osteopathic;
XX antineoplastic; antirheumatic; vaccine; immunisation; infectious disease;
XX anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
XX graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
XX Alzheimer's disease; osteoporosis; rheumatoid arthritis;
XX inflammatory autoimmune disease.
XX Bacteriophage Qbeta.
OS Synthetic.
XX
XX WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
XX
XX 14-SEP-2001; 2001US-0318967P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M, Storni T, Lechner F;
XX
XX WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
XX or a virus-like particle, enhancing anti-viral protection in an animal,
XX PT or immunizing or treating tumors or infectious diseases, e.g. viral
XX PT infections.
XX
XX Disclosure; Page 180-181; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
XX response against an antigen or a virus-like particle in an animal. (C)
XX comprises a virus-like particle (VLP) bound to at least one antigen, or a
XX VLP capable of being recognised by the immune system of the animal. Also
XX described: (1) enhancing an immune response against an antigen or a VLP
XX in an animal comprising introducing (C) into the animal; (2) vaccines
XX comprising (C) together with a pharmaceutical diluent, carrier or
XX excipient; (3) immunising or treating an animal comprising administering
XX the vaccine to the animal, or priming or boosting a T cell response in
XX the animal by administering the vaccine; and (4) enhancing anti-viral
XX protection in an animal comprising introducing (C) into the animal. (C)
XX has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
XX antiallergic, immunosuppressive, antiaddictive, antitumorigenic,
XX antihypertensive, antidiabetic, neuroprotective, nootropic, osteopathic,
XX antineoplastic and antirheumatic activities. (C) or the vaccines can be
XX used for enhancing an immune response against an antigen or a VLP in an
XX animal, enhancing anti-viral protection in an animal, or immunising or
XX treating tumors and infectious diseases such as viral, bacterial,
XX parasitic or fungal infections. The vaccine compositions are also useful
XX for preventing or treating allergies, drug addiction, graft-versus-host
XX disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
XX Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
XX autoimmune disease. ACC69852 to ACC69852 and ABR56453 to ABR56453
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ
Query Match 100.0%; Score 663; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,7e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 AKLETVTLGKIGKDGKQTLVLPNGVNPFTNGVSLSQAGAVPALEKRVTVSVSOPSRNRK 60
OY 61 NYKQVQKIQNPACTANGSCPSVTRQKAVTVTSFTQYSDERAFVTEIAALIASPL 120
DB 61 NYKQVQKIQNPACTANGSCPSVTRQKAVTVTSFTQYSDERAFVTEIAALIASPL 120
OY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132
RESULT 4
ABU09690 standard; protein; 132 AA.
ID ABU09690
XX
XX AC ABU09690;
XX
XX DT 03-JUL-2003 (first entry)
XX
XX DE Bacteriophage Qbeta mutant coat protein #2.
XX
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
XX cardiatic; nephroretropic; ophtalmological; immunostimulant; vaccine;
XX angiotensin peptide moiety carrier conjugate; angiotensin peptide;
XX renin-activated angiotensin system; hypertension; stroke; infarction;
XX congestive heart failure; kidney failure; retinal haemorrhage; mutant;
XX mutein.
XX
XX Bacteriophage Qbeta.
OS WO2003031466-A2.
XX
XX 17-APR-2003.
XX
XX 07-OCT-2002; 2002WO-EP011219.
XX
XX 05-OCT-2001; 2001US-0326998P.
XX
XX 07-NOV-2001; 2001US-0311045P.
XX
XX 18-JAN-2002; 2002US-00050902.
XX
XX 21-JAN-2002; 2002WO-IB000166.
XX
XX 19-JUL-2002; 2002US-0396537P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M;
XX
XX WPI; 2003-430264/40.
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
XX an angiotensin peptide moiety, useful for treating or preventing a
XX disorder associated with renin-activated angiotensin, e.g. hypertension
XX or infarction.
XX
XX Claim 20; Page 94; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
XX comprising: (a) a carrier with at least one first attachment site; and
XX (b) at least one angiotensin peptide moiety with at least one second
XX attachment site. The angiotensin peptide moiety and compositions
XX comprising them are useful for immunising an animal against an
XX angiotensin peptide, and for treating or preventing a physical disorder
XX associated with renin-activated angiotensin system such as hypertension,
XX stroke, infarction, congestive heart failure, kidney failure, and retinal
XX haemorrhage. The conjugate is also useful for inducing immune responses,
XX including producing antibodies. This is the amino acid sequence of a
XX mutant bacteriophage Qbeta coat protein used in the preparation of the
XX vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ
Query Match 100.0%; Score 663; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,7e-69;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60
 DB 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRKRYADVTFSTFYQSTDEBRARFVTELAALLASPL 120
 DB 61 NYKVQVKIOMPACTANGSCDPSVTRKRYADVTFSTFYQSTDEBRARFVTELAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 5
 ABR44556
 ID ABR44556 standard; protein; 132 AA.
 AC ABR44556;
 DT 25-JUL-2003 (first entry)

DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:24.

KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virocidic; antibacterial;
 KW immune response; immunisation; allergy; tumor; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Bacteriophage Qbeta.
 OS Synthetic.
 XX WO2003024481-A2.
 PN 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-IB004132.
 PF 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER) MAURER P.
 PA (TISSOT) TISSOT A.
 PA (SCHWAB) SCHWAB K.
 PA (MEIER) MEIERINK E.
 PA (LIPPO) LIPPOWSKY G.
 PA (PUMP) PUMPENS P.
 PA (CIEL) CIELENS I.
 PA (REINH) REINHOF A R.

XX MAURER P, TISSOT A, SCHWAB K, MEIERINK E, LIPPOWSKY G;
 PI Pumpens P, Cielens I, Reinhold R, Bachmann MF, Storni T;
 PT WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.

XX Disclosure; Page 260; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virocidic and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention

CC Sequence 132 AA;
 SQ

Query Match 100.0%; Score 663; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60
 DB 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRKRYADVTFSTFYQSTDEBRARFVTELAALLASPL 120
 DB 61 NYKVQVKIOMPACTANGSCDPSVTRKRYADVTFSTFYQSTDEBRARFVTELAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 6
 ADD24131
 ID ADD24131 standard; protein; 132 AA.
 AC ADD24131;
 DT 15-JAN-2004 (first entry)

DE Bacteriophage Qbeta coat protein mutant Qbeta-243.

KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob disease; coat protein; mutant; mutagen.

XX Synthetic.
 OS Bacteriophage Qbeta.
 OS WO2003059386-A2.
 PN 24-JUL-2003.
 PD 17-JAN-2003; 2003WO-EP000460.
 PF 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 PI WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.

PT Hodgkin's lymphoma.
 XX
 PS Disclosure; SEQ ID NO 24; 245bp; English.
 XX
 CC The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medications, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 663; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 DB 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVRELAALLASPL 120
 DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVRELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132
 RESULT 9
 ADJ36314
 ID ADJ36314 standard; protein; 132 AA.
 XX
 AC ADJ36314;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Bacteriophage Qbeta coat protein virus-like particle mutant K13R.
 XX
 KW anti-allergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage Qbeta;
 KW coat protein; VLP; adjuvant; mutant; muten.
 OS Bacteriophage Qbeta.
 XX
 PN WO2004000351-A1.
 XX
 PD 31-DEC-2003.
 XX
 PF 20-JUN-2003; 2003WO-EP006541.
 XX
 PR 20-JUN-2002; 2002US-0389898P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Renner WA;
 XX
 DR WPI; 2004-108361/11.
 XX
 PT New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with
 PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
 XX
 PS Disclosure; SEQ ID NO 15; 252bp; English.
 XX
 CC The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
 CC coat protein mutant, a virus like particle (VLP) that can be used in the
 CC adjuvant of the invention.
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 663; DB 8; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 DB 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVRELAALLASPL 120
 DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVRELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132
 RESULT 10
 ADJ67160
 ID ADJ67160 standard; protein; 132 AA.
 XX
 AC ADJ67160;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Phage Qbeta coat protein mutant Qbeta 243 for antigen display array.
 XX
 KW anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 KW antigenic array.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 PN WO2004009124-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007849.
 XX
 PR 19-JUL-2002; 2002US-0396638P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Fulurija A;
 XX
 DR WPI; 2004-132866/13.
 XX
 PT New composition comprising a core particle having a first attachment site
 PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
 PT peptide having a second attachment site, useful for treating obesity.
 XX
 PS Disclosure; SEQ ID NO 18; 175bp; English.
 XX
 CC The invention relates to a new composition comprising: (i) a core
 CC particle with at least one first attachment site; and (ii) at least one
 CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
CC peptide, and where the second attachment site being consisting of an
CC attachment site not naturally occurring with the antigen or antigenic
CC determinant and an attachment site naturally occurring with the antigen
CC or antigenic determinant, where the second attachment site is capable of
CC association to the first attachment site, and where the ghrelin or a
CC ghrelin peptide and the core particle interact through the association to
CC form an ordered and repetitive antigen array. The composition is useful
CC for treating obesity. The repetitive array may form part of a phage or
CC bacterial display array. This peptide corresponds to a Bacteriophage
CC Qbeta coat protein mutant which can used as part of the repetitive or
CC antigenic array.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 663; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.7e-69; Indels 0; Gaps 0;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGKIGKDGKQTLVNPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
DB 1 AKLEVTTLGKIGKDGKQTLVNPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132
RESULT 11
ADK52194
ID ADK52194 standard; protein; 132 AA.
XX
AC ADK52194;
XX
DT 20-MAY-2004 (first entry)
XX
DE Bacteriophage Qbeta coat protein mutant N10K.
XX
KM neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
KM core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
KM coat protein; CP; mutant; mutein.
OS Bacteriophage Qbeta.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 10 /note= "Wild type Asn substituted by Lys"
FT
FT
PN WO2004016282-A1.
XX
PD 26-FEB-2004.
XX
PF 18-JUL-2003; 2003WO-EP007864.
XX
PR 19-JUL-2002; 2002US-0396639P.
PR 15-MAY-2003; 2003US-0470432P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
PI Bachmann M, Tisot A, Ortman R, Lucend R, Staufendiel M,
PI Frey P,
XX
XX WPI, 2004-203731/19.
XX
XX Composition comprising a core particle with at least one attachment site,
PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
PT such as Alzheimer's disease.

XX
PS Example 1; SEQ ID NO 18; 184bp; English.
XX
XX The invention describes a novel composition comprising a virus-like core
XX particle with at least one attachment site, and an antigenic amyloid beta
XX 1-6 peptide. The new composition comprises: a core particle with at least
XX one first attachment site; and at least one antigen or antigenic
XX determinant with at least one second attachment site, where the antigen
XX or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
XX second attachment site comprises: an attachment site not naturally
XX occurring with the antigen or antigenic determinant; or an attachment
XX site naturally occurring with the antigen or antigenic determinant. The
XX second attachment site is capable of association to the first attachment
XX site and the beta 1-6 peptide and the core particle interact through the
XX association to form an ordered and repetitive antigen array. The
XX composition is useful for the manufacture of a medicament for treating
XX Alzheimer's disease and related diseases. This is the amino acid sequence
XX of an RNA bacteriophage Qbeta coat protein mutant that can be used in the
XX preparation of the compositions and vaccines of the invention.
SQ Sequence 132 AA;
Query Match 100.0%; Score 663; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.7e-69; Indels 0; Gaps 0;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGKIGKDGKQTLVNPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
DB 1 AKLEVTTLGKIGKDGKQTLVNPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132
RESULT 12
ABG94316
ID ABG94316 standard; protein; 132 AA.
XX
AC ABG94316;
XX
DT 29-AUG-2003 (revised)
DT 10-DEC-2002 (first entry)
XX
DE P08240 protein.
XX
KM Human; mouse; rat; antimicrobial; antifungal; immunomodulatory;
KM cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KM vaccine; infectious disease.
OS unidentified bacteriophage.
OS
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-1B000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288548P.
PR 05-OCT-2001; 2001US-0326988P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Renner WA, Bachmann M, Tisot A, Maurer P, Lechner F, Sebbel P,
PI Ploesek C,
XX
XX WPI, 2002-627351/67.

XX	
PT	Molecular antigen array used in the production of vaccines for infectious diseases.
PT	

Claim 18; Page 144; 441pp; English

CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organism comprising
CC at least one first attachment site, where the organism is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is anyloid beta peptide
CC (A β 1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Obeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention. (Updated on 29
CC -Aug-2003 to standardise OS field)

SQ Sequence 132 AA;

Query Match	98.8%;	Score 655;	DB 5;	Length 132;
Best Local Similarity	98.5%;	Pred. No. 2.4e-68;		
Matches 130; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0

[illegible]

RESULT 13

ID ABG94320 standard; protein; 132 AA.

AC ABG943207

DT	29-AUG-2003	(revised)
DT	10-DEC-2002	(first entry)

DE pQB251 protein.

KM Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KM cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array
KM vaccine; infectious disease.

OS unidentified bacteriophage.

PN WO200256905-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002WO-IB000166

AA 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI	Renner WA,	Bachmann M,	Tissot A,	Maurer P,	Lechner F,	Sebbel P,
PI	Plosek C;					

WPI; 2002-627351/67.

PT Molecular antigen array used in the production of vaccines for infectious PT diseases.

PS Claim 18; Page 426; 441pp; English

CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is any/oid beta peptide
CC (Abeta-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cyostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention. (Updated on 29
CC -Aug-2003 to standardise OS field)

SQ Sequence 132 AA;

Query Match	98.8%	Score 655;	DB 5;	Length 132;
Best Local Similarity	98.5%	Pred. No. 2.4e-68;		
Matches 130; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	ACLEVTYTLGKIKDDGQTLVNLNPRGVNPTNGVASLSQAGAVPLERKVTVSVSQPSRNK	60
Db	1	ACLEVTYTLGNICKDGGQTLVNLNPRGVNPTNGVASLSQAGAVPLERKVTVSVSQPSRNK	60
QY	61	NKKVQYKIONPRACTANGSCDPSVTRQKADVTFSFYQSTDEERAFVETELALIASPL	120
Db	61	NKKVQYKIONPRACTANGSCDPSVTRQKADVTFSFYQSTDEERAFVETELALIASPL	120
QY	121	LIDAIQOLNPAY	132
Db	121	LIDAIQOLNPAY	132

RESULT 14

ID	ABG80632	standard; protein; 132 AA.
vv		

AC ABG80632

DT 29-NOV-2002 (first entry)
xxDE Bacteriophage ϕ -beta A1 coat protein mutant ϕ beta-259.

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 10.3622 Seconds

(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-7

Perfect score: 663

Sequence: 1 AKETVTLGKIGKDGKQTLV.....ALLASPLLDALDQLNPAY 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	12.7	626	4 US-09-485-717-2	Sequence 2, Appli
2	84.5	12.7	626	4 US-09-948-722-2	Sequence 2, Appli
3	72.5	10.9	916	4 US-09-252-991A-23637	Sequence 23637, A
4	72	10.9	409	4 US-09-328-352-4249	Sequence 4249, A
5	70.5	10.6	502	4 US-09-270-767-44620	Sequence 44620, A
6	70.5	10.6	2042	4 US-09-077-098A-6	Sequence 6, Appli
7	70	10.6	233	3 US-08-725-459B-45	Sequence 45, Appli
8	70	10.6	341	3 US-08-725-459B-44	Sequence 44, Appli
9	70	10.6	434	3 US-08-725-459B-42	Sequence 42, Appli
10	69.5	10.5	129	1 US-08-090-148-1	Sequence 11, Appli
11	69	10.4	273	3 US-08-235-836C-11	Sequence 89, Appli
12	69	10.4	273	3 US-08-235-836C-89	Sequence 89, Appli
13	68.5	10.3	383	1 US-09-045-186-2	Sequence 2, Appli
14	68.5	10.3	384	1 US-08-235-144-4	Sequence 4, Appli
15	68.5	10.3	384	2 US-08-555-268A-15	Sequence 15, Appli
16	68.5	10.3	384	3 US-09-200-673-15	Sequence 15, Appli
17	68.5	10.3	384	4 US-10-013-846-4	Sequence 9, Appli
18	68.5	10.3	384	4 US-09-708-392-9	Sequence 3, Appli
19	68.5	10.3	384	5 PCT-US93-05039-3	Sequence 3, Appli
20	68.5	10.3	411	3 US-08-817-869-3	Sequence 3, Appli
21	68.5	10.3	411	5 PCT-US95-14377-3	Sequence 3, Appli
22	68.5	10.3	733	4 US-09-248-796A-16565	Sequence 16565, A
23	68	10.3	316	4 US-09-270-767-43925	Sequence 43925, A
24	68	10.3	316	4 US-09-270-767-59331	Sequence 59331, A
25	67.5	10.2	424	3 US-09-173-581-7	Sequence 7, Appli
26	67.5	10.2	424	3 US-09-420-915-7	Sequence 7, Appli
27	67.5	10.2	1328	3 US-08-781-891-76	Sequence 76, Appli

28	67.5	10.2	1328	4 US-09-618-166-76	Sequence 76, Appli
29	66.5	10.0	141	4 US-09-248-796A-16789	Sequence 16789, A
30	66.5	10.0	279	3 US-08-397-411-13	Sequence 13, Appli
31	66.5	10.0	569	4 US-09-248-796A-20249	Sequence 20249, A
32	66.5	10.0	818	4 US-09-252-991A-16691	Sequence 16691, A
33	66	10.0	345	3 US-08-856-253-7	Sequence 7, Appli
34	66	10.0	737	4 US-09-071-035-460	Sequence 460, App
35	66	10.0	933	3 US-08-293-728-2	Sequence 2, Appli
36	66	10.0	936	4 US-09-421-868-2	Sequence 2, Appli
37	66	10.0	936	4 US-08-956-171B-5249	Sequence 5249, Ap
38	66	10.0	936	4 US-08-781-986A-5249	Sequence 5249, Ap
39	66	10.0	1036	2 US-08-720-484A-5	Sequence 5, Appli
40	66	10.0	1036	3 US-08-953-823A-5	Sequence 5, Appli
41	66	10.0	1036	4 US-09-398-239-5	Sequence 5, Appli
42	66	10.0	1036	4 US-09-560-876A-5	Sequence 5, Appli
43	66	10.0	1065	4 US-09-560-876A-6	Sequence 6, Appli
44	66	10.0	1281	2 US-08-843-530B-6	Sequence 6, Appli
45	66	10.0	1281	4 US-09-636-728-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-09-485-717-2
Sequence 2, Application US/09485717
Patent No. 6673353
GENERAL INFORMATION:
APPLICANT: Kaufmann, Stefan
APPLICANT: Hess, Jürgen
TITLE OF INVENTION: Tuberculosis Vaccine
FILE REFERENCE: 16862PUS
CURRENT APPLICATION NUMBER: US/09/485,717
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: EP 97114614.7
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PCT/EP98-05109
PRIOR FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2
Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best Local Similarity 22.7%; Pred. No. 0.14;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGKQTLV-----NPRGVNPTNGVASLSQAG-----VPALEKRV 48
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 KDGNEYIVVEKKKSINNNADIQVNAISLTFPGALVANSSEVENQDVLVKKRDSL 197
QY 49 TVSSQSPSRKKKVKQVQKQNPACTANGSCDSVTR-----QKADYTFSTQVSTD 102
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 198 TLSDLPGMTQNDKRIYK--NATKSNVNNNAVTLVERMNEKVAQAAYPNVS--AKIDYD 252
QY 103 EERAFVTELLA 114
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 DEMAYSESQILA 264
RESULT 2
US-09-948-722-2
Sequence 2, Application US/09948722
Patent No. 6776993
GENERAL INFORMATION:
APPLICANT: Kaufmann, Stefan H. E.
APPLICANT: Hess, Jürgen
TITLE OF INVENTION: Tuberculosis Vaccine
```

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best Local Similarity 22.7%; Pred. No. 0.14;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGKQTLV-----NPRGVNPTNGVASLSQAGA-----VPALRKRV 48
DB 138 KQNEIYVEKKKKKINSNNADIOVNNALISLTYPGALVKANSEVENOPDVLVYKRDSTL 197
QY 49 TVSVSPSRNKKYKQVIONPACTANGSCDPSVTR-----OKYADVTFSTQYSTD 102
DB 198 TLTIDLPKNTNDONKTVK--NATKSNVNNVATTLVERNKKYQAYPRVVS---AKIDYD 252
QY 103 EERAFVTEIAA 114
DB 253 DEMAYSESQLIA 264

RESULT 3
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match 10.9%; Score 72.5; DB 4; Length 916;
Best Local Similarity 22.9%; Pred. No. 8.6; Mismatches 53; Indels 21; Gaps 4;
Matches 27; Conservative 17

QY 9 GKIGKDG-----KQTLVNRGVNPTNGVASLSQAGAVPALRKRVTVSVS-----QP 55
DB 789 GLGGBEALRLRLRAIVQARRIDPFGGLAALPVGGLPALBQEDPAFGSLDORWQA 848
QY 56 SRNKKYKQVIONPACT--TANGSCDPSVTRQKYADVTFSFTQYSTDEBAFVRT 110
DB 849 EERGAIFYRAQBSAHEHPCRSIEANADCPISADAGK-----PWTIFSDATRWALRT 901

RESULT 4
US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-039A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match 10.9%; Score 72; DB 4; Length 409;
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 26; Conservative 18; Mismatches 44; Indels 16; Gaps 4;

QY 26 VNPTNGVASLSQAGAVPALRKRVTVSVSPSRNKKYKQVIONPACTANGSCDPSV 84
DB 137 VNPVDGTTPI-----IAKPNQRLTIRDLAPGRGNS--AIAYLRETFNNALVPE 188
QY 85 TRQKYADVTFSFTQYSTDEBAFVRTLEALLASPLIDAIDQL 128
DB 189 TAKPYSEITP-----EENVESYKTIAMLMKASKQIIDLDPOL 225

RESULT 5
US-09-270-767-44620
Sequence 44620, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44620
LENGTH: 502
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44620

Query Match 10.6%; Score 70.5; DB 4; Length 502;
Best Local Similarity 24.2%; Pred. No. 6;
Matches 29; Conservative 20; Mismatches 52; Indels 19; Gaps 4;

QY 18 TLVNRGVNPTNGVASLSQAGAVPALRKRVTVSVSP-----SRNKKYKQVION 70
DB 258 TIANV---ISPSPTPPQPIVEPVEQVENSVTIVASPEVPVAXARNDXRQSTRSTIK 314
QY 71 PRACTANGSCDPSVTRQKYADVTFSFTQ-----YSTDEBAFVRT--ELAALLASPL 121
DB 315 AXVVKYFSCSTSSATHTSCISVYSOSLGPSPILGAXDKDFVTLKPLATFTISSPWL 374

RESULT 6
US-09-077-098A-6
Sequence 6, Application US/09077098A
Patent No. 6544519
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
SAKAGUCHI, Masaaki
MATSUO, Kazuo
HAWADA, Fukunaburo

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..233
OTHER INFORMATION: /note= "amino acids 202-434 of C.
OTHER INFORMATION: "elegans"
US-08-725-459B-45

Query Match          10.6%; Score 70; DB 3; length 233;
Best local Similarity 32.6%; Pred. No. 2.1;
Matches   31; Conservative   13; Mismatches    37; Indels   14; Gaps    5

QY      2 KLETVTLGKIG-----DGKQTVLNDRGVNPFTNGVASLSQAGV--PALERKVTVSVS 53
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db       116 KLEMTL-SRIGKSNSAQSGRGQTWVIDWAHTR----VRSKSFFTVYDSDVKMSATPSAL 170
QY      54 QPSRRNKYKYQVKIQLONPACTANGSCDPSTYRK 88
        |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db       171 QLSQARKNVKIEGKAQLRT-ITPRGGVPTSRSR 204

RESULT 8
US-08-725-459B-44
Sequence 44, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAMAY, RONALD C.
APPLICANT: CONAMAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIP: 75201-6507
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 44
```

SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..341
OTHER INFORMATION: /note= "amino acids 94-434 of C."
US-08-725-459B-44

Query Match 10.6%; Score 70; DB 3; Length 341;
Best Local Similarity 32.6%; Pred. No. 3.8;
Matches 31; Conservative 13; Mismatches 37; Indels 14; Gaps 5;

QY 2 KLEVTYLGKIGK-----DGKQTLVLPNGVPTNGVSLSQAGV--PALEKRVTVSVS 53
DB 224 KLEMLT-SRIGKNSAOSQGRQTVWDMAHTR----VSKSFPTVKDSQVMSATPSAL 278

QY 54 QPSRRKRYKVQVKIQNPACTANGSCDPSVTROK 88
DB 279 QLSQARKVKIKGKAQLRT-ITPRGGVPTSTRSR 312

RESULT 9
US-08-725-459B-42
Sequence 42, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIP: 75201-6507
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..434
OTHER INFORMATION: /note= "entire amino acid sequence
of C. elegans"
US-08-725-459B-42

Query Match 10.6%; Score 70; DB 3; Length 434;

Best Local Similarity 32.6%; Pred. No. 5.5;
Matches 31; Conservative 13; Mismatches 37; Indels 14; Gaps 5;
QY 2 KLEVTYLGKIGK-----DGKQTLVLPNGVPTNGVSLSQAGV--PALEKRVTVSVS 53
DB 317 KLEMLT-SRIGKNSAOSQGRQTVWDMAHTR----VSKSFPTVKDSQVMSATPSAL 371

QY 54 QPSRRKRYKVQVKIQNPACTANGSCDPSVTROK 88
DB 372 QLSQARKVKIKGKAQLRT-ITPRGGVPTSTRSR 405

RESULT 10
US-08-090-148-1
Sequence 1, Application US/08090148
Patent No. 5534257
GENERAL INFORMATION:
APPLICANT: Mastico, Robert Allan
APPLICANT: Stockley, Peter George
APPLICANT: Talbot, Simon John
TITLE OF INVENTION: Antigen-Presenting Capsid with
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roseman & Colin
STREET: 575 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10022-2585
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44MB
COMPUTER: IBM PS2-486
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,148
FILING DATE: 08/11/93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101550.3
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/22/92
ATTORNEY/AGENT INFORMATION:
NAME: Nissenbaum, Israel
REGISTRATION NUMBER: 27,582
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8636
TELEFAX: (212) 940-6404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: NOT RELEVANT
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: VIRUS
FEATURE:
NAME/KEY: Coat protein from MS2-RNA
NAME/KEY: bacteriophage
LOCATION: location 1 through 129 below
LOCATION: represents entire MS2 coat
LOCATION: protein in the published
LOCATION: sequence.
PUBLICATION INFORMATION:
AUTHORS: Min Jou, W.; Haegeman, G.;
AUTHORS: Ysebaert, M.; Fiers, W.
TITLE: Nucleotide sequence of the
TITLE: gene coding for the
TITLE: bacteriophage MS2 coat protein
JOURNAL: Nature

VOLUME: 237
PAGES: 82-88
DATE: 1972
US-08-090-148-1

Query Match 10.5%; Score 69.5; DB 1; Length 129;

Best Local Similarity 25.0%; Pred. No. 0.94; Mismatches 43; Indels 13; Gaps 2;

Matches 24; Conservative 16; Mismatches 43; Indels 13; Gaps 2;
Qy 27 NPTNGVA-----SISQAGVPALEKRVTVSVSPSRNKYKVQKIONPTACTANGSC 80
Db 24 NPAAGVAEIKSSNSQA-----YKTCVRSQSAQNRKTKTIKVEKATQTVGVE 76
Qy 81 DSVTRQKYADYTFSTQYSTDEBRAVTELAAL 116
Db 77 LPVAAWRSYLMELTRIPATNSDCELIYKAMQGL 112

RESULT 11

US-08-235-836C-11

Sequence 11, Application US/08235836C

Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

STREET: Brookhaven National Laboratory

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/148,191

ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Margaret C.

REGISTRATION NUMBER: 25,324

REFERENCE/DOCKET NUMBER: BNL93-28A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 282-7338

TELEFAX: (516) 282-3729

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-235-836C-11

Query Match 10.4%; Score 69; DB 3; Length 273;

Best Local Similarity 28.8%; Pred. No. 3.6;

Matches 23; Conservative 12; Mismatches 35; Indels 10; Gaps 3;

Qy 5 TTTTGGK-IGKDGKQTLVNPNGVNPNGVASISQAGVPALEKRVTVSVSPSRNR----- 59
Db 184 TTTLSKEIKAKSGEVVAL-----NDNTNTQATKTKTGAMDSKSTLTISVNSKTTQVLVFT 238
Qy 60 KNYKVQVKIONPTACTANGS 79
Db 239 KQYITTVKQYDSAGTNLEGT 258

RESULT 12

US-08-235-836C-89

Sequence 89, Application US/08235836C

Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

STREET: Brookhaven National Laboratory

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/148,191

ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Margaret C.

REGISTRATION NUMBER: 25,324

REFERENCE/DOCKET NUMBER: BNL93-28A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 282-7338

TELEFAX: (516) 282-3729

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-235-836C-89

Query Match 10.4%; Score 69; DB 3; Length 273;

Best Local Similarity 28.8%; Pred. No. 3.6;

Matches 23; Conservative 12; Mismatches 35; Indels 10; Gaps 3;

Qy 5 TTTTGGK-IGKDGKQTLVNPNGVNPNGVASISQAGVPALEKRVTVSVSPSRNR----- 59
Db 184 TTTLSKEIKAKSGEVVAL-----NDNTNTQATKTKTGAMDSKSTLTISVNSKTTQVLVFT 238
Qy 60 KNYKVQVKIONPTACTANGS 79
Db 239 KQYITTVKQYDSAGTNLEGT 258

COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36, 808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-045-186-2

Query Match 10.3%; Score 68.5; DB 3; Length 383;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRVTVSVQPSRRKRYQVK 67
DB 138 RHQLINPGRWRPNRRHAYVGIWVLA VASSLPFLIYQ--VMTDEPFQN----- 186

QY 68 IQNPTACTANGSCDPSYTRQKYADVTFSPFYQSTDEBFAFRTEAL 115
DB 187 -----VTLDAVKQKYVCFDQFSDSHRLSTYTLVLVL 218

RESULT 14
US-08-232-144-4
Sequence 4, Application US/08232144
Patent No. 5571695
GENERAL INFORMATION:
APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
APPLICANT: SHINE, John
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F199, Ernst & Kutz
STREET: 555 13th St, N.W., Suite 701-East
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,144
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-144-4

Query Match 10.3%; Score 68.5; DB 1; Length 384;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRVTVSVQPSRRKRYQVK 67
DB 138 RHQLINPGRWRPNRRHAYVGIWVLA VASSLPFLIYQ--VMTDEPFQN----- 186

QY 68 IQNPTACTANGSCDPSYTRQKYADVTFSPFYQSTDEBFAFRTEAL 115
DB 187 -----VTLDAVKQKYVCFDQFSDSHRLSTYTLVLVL 218

RESULT 15
US-08-555-268A-15
Sequence 15, Application US/08555268A
Patent No. 5958709
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,268A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44743-Z/JPM/WAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0526
TELEFAX: (212) 278-0400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-555-268A-15

Query Match 10.3%; Score 68.5; DB 2; Length 384;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRVTVSVQPSRRKRYQVK 67
DB 138 RHQLINPGRWRPNRRHAYVGIWVLA VASSLPFLIYQ--VMTDEPFQN----- 186

Oy 68 IONPTACTANGSCDPSYTRQKYADVTFFSTQYSTDEBAFVRELAAL 115
Db 187 -----VTLDAYKDKYVCFDQFPSSSHRLSYTTLALVL 218

Search completed: January 4, 2005, 09:35:44
Job time : 11.3622 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-7
Perfect score: 663
Sequence: 1 AKLEVTITGKIGKDGKQTLV.....AALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1539051 seqs, 359727711 residues
Total number of hits satisfying chosen parameters: 1539051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: Published Applications_AA.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	132	US-10-243-739-24	Sequence 24, Appl
2	663	100.0	132	US-10-244-065-24	Sequence 24, Appl
3	663	100.0	132	US-10-289-454-24	Sequence 24, Appl
4	663	100.0	132	US-10-050-902-256	Sequence 256, App
5	663	100.0	132	US-10-050-898-256	Sequence 256, App
6	663	100.0	132	US-10-346-190-24	Sequence 24, Appl
7	663	100.0	132	US-10-465-811-15	Sequence 15, Appl
8	663	100.0	132	US-10-289-456-24	Sequence 24, Appl
9	663	100.0	132	US-10-622-064-7	Sequence 7, Appl
10	663	100.0	132	US-10-622-124-18	Sequence 18, Appl
11	663	100.0	132	US-10-622-087-18	Sequence 18, Appl
12	655	98.8	132	US-10-243-739-23	Sequence 23, Appl
13	655	98.8	132	US-10-243-739-26	Sequence 26, Appl

14	655	98.8	132	US-10-244-065-23	Sequence 23, Appl
15	655	98.8	132	US-10-244-065-26	Sequence 26, Appl
16	655	98.8	132	US-10-289-454-23	Sequence 23, Appl
17	655	98.8	132	US-10-289-454-26	Sequence 26, Appl
18	655	98.8	132	US-10-050-902-255	Sequence 255, App
19	655	98.8	132	US-10-050-902-259	Sequence 259, App
20	655	98.8	132	US-10-050-898-255	Sequence 255, App
21	655	98.8	132	US-10-050-898-259	Sequence 259, App
22	655	98.8	132	US-10-346-190-23	Sequence 23, Appl
23	655	98.8	132	US-10-346-190-26	Sequence 26, Appl
24	655	98.8	132	US-10-465-811-14	Sequence 14, Appl
25	655	98.8	132	US-10-465-811-17	Sequence 17, Appl
26	655	98.8	132	US-10-289-456-23	Sequence 23, Appl
27	655	98.8	132	US-10-289-456-26	Sequence 26, Appl
28	655	98.8	132	US-10-622-064-6	Sequence 6, Appl
29	655	98.8	132	US-10-622-064-9	Sequence 9, Appl
30	655	98.8	132	US-10-622-124-17	Sequence 17, Appl
31	655	98.8	132	US-10-622-087-17	Sequence 17, Appl
32	655	98.8	132	US-10-622-087-20	Sequence 20, Appl
33	655	98.8	132	US-10-243-739-25	Sequence 25, Appl
34	652	98.3	132	US-10-243-739-25	Sequence 25, Appl
35	652	98.3	132	US-10-243-739-27	Sequence 27, Appl
36	652	98.3	132	US-10-244-065-10	Sequence 10, Appl
37	652	98.3	132	US-10-244-065-25	Sequence 25, Appl
38	652	98.3	132	US-10-244-065-27	Sequence 27, Appl
39	652	98.3	132	US-10-289-454-10	Sequence 10, Appl
40	652	98.3	132	US-10-289-454-25	Sequence 25, Appl
41	652	98.3	132	US-10-289-454-27	Sequence 27, Appl
42	652	98.3	132	US-10-050-902-159	Sequence 159, App
43	652	98.3	132	US-10-050-902-257	Sequence 257, App
44	652	98.3	132	US-10-050-902-258	Sequence 258, App
45	652	98.3	132	US-10-050-902-258	Sequence 258, App

ALIGNMENTS

RESULT 1
US-10-243-739-24
; Sequence 24, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-24

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTITGKIGKDGKQTLVNPGRVNTNGVASISQAGVPALEKRTVSQPSRRK 60
DB 1 AKLEVTITGKIGKDGKQTLVNPGRVNTNGVASISQAGVPALEKRTVSQPSRRK 60
QY 61 NYKVVQKIONTPACTANGSCPSVTRKQYADVTSTFTYSTDERAFVTELAALIASPL 120
DB 61 NYKVVQKIONTPACTANGSCPSVTRKQYADVTSTFTYSTDERAFVTELAALIASPL 120
QY 121 LIDALDQNPAY 132

Db 121 LIDAIIDQINPAY 132

RESULT 2

US-10-244-065-24
Sequence 24, Application US/10244065
Publication No. US20030099668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tisbet, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Weijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-24

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4,3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNK 60
DB 1 AKLEVTYLGKIGDKGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNK 60
QY 61 NYKVQYKIQNPACTANGSCDPSVTROKADYVTFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQYKIQNPACTANGSCDPSVTROKADYVTFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 3

US-10-289-454-24
Sequence 24, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
PRIOR FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-243
US-10-289-454-24

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4,3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNK 60
DB 1 AKLEVTYLGKIGDKGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNK 60
QY 61 NYKVQYKIQNPACTANGSCDPSVTROKADYVTFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQYKIQNPACTANGSCDPSVTROKADYVTFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 4

US-10-050-902-256
Sequence 256, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tisbet, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Seibel, Peter
APPLICANT: Ploesek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 256
LENGTH: 132
TYPE: PRT
ORGANISM: Qb 243
US-10-050-902-256

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4,3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AKLEVTYLGKIGDKGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNK 60
QY 61 NYKVQYKIQNPACTANGSCDPSVTROKADYVTFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQYKIQNPACTANGSCDPSVTROKADYVTFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

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RESULT 5
US-10-050-898-256
; Sequence 256, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Orlmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Db 243
US-10-050-898-256

Query Match      100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASLSQAGAVPALKRTVTSVSQPSRRK 60
Db      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASLSQAGAVPALKRTVTSVSQPSRRK 60
Qy      61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDEERAFVTELAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDEERAFVTELAALLASPL 120
Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

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; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Db 243
US-10-346-190-24

Query Match      100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASLSQAGAVPALKRTVTSVSQPSRRK 60
Db      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASLSQAGAVPALKRTVTSVSQPSRRK 60
Qy      61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDEERAFVTELAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDEERAFVTELAALLASPL 120
Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 8
US-10-289-456-24
; Sequence 24, Application US/10289456

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Publication No. US2004003211A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 243 mutant
US-10-289-456-24

Query Match      100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
DB      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
QY      61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDERAFVRELAALASPL 120
DB      61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDERAFVRELAALASPL 120
QY      121 LIDAIIDQINPAY 132
DB      121 LIDAIIDQINPAY 132

RESULT 9
US-10-622-064-7
Sequence 7, Application US/10622064
Publication No. US2004005904A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,575
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-622-064-7

Query Match      100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
DB      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
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DB      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
QY      61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDERAFVRELAALASPL 120
DB      61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDERAFVRELAALASPL 120
QY      121 LIDAIIDQINPAY 132
DB      121 LIDAIIDQINPAY 132

RESULT 10
US-10-622-124-18
Sequence 18, Application US/10622124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fuhurija, Alma
TITLE OF INVENTION: Chreilin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,638
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-622-124-18

Query Match      100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
DB      1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
QY      61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDERAFVRELAALASPL 120
DB      61 NYKVQVKIONPTACTANGSCDPSVTRKXADVTFSFTQYSTDERAFVRELAALASPL 120
QY      121 LIDAIIDQINPAY 132
DB      121 LIDAIIDQINPAY 132

RESULT 11
US-10-622-087-18
Sequence 18, Application US/10622087
Publication No. US20040141984A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tissot, Alain
APPLICANT: Ottmann, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Staufenbiel, Matthias
APPLICANT: Frey, Peter
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
```

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; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-622-087-18

```

Query Match	100.0%;	Score 663;	DB 16;	Length 132;
Best Local Similarity	100.0%;	Pred. No. 4.3e-66;		
Matches 132; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	AKLEVTITGKIGKDGQOTLVINBPRGVPNTNGVASTSQAGVNPALBKRVTVSVSQPSNRK	60
Db	1	AKLEVTITGKIGKDGQOTLVINBPRGVPNTNGVASTSQAGVNPALBKRVTVSVSQPSNRK	60
Qy	61	NYKVGVKIQNPACTANGSCDPSVTROKADADVTSEFQVSTDBERAFVRETELAAALASPL	120
Db	61	NYKVGVKIQNPACTANGSCDPSVTROKADADVTSEFQVSTDBERAFVRETELAAALASPL	120
Qy	121	LIDAIQOLNPAY	132
Db	121	LIDAIQOLNPAY	132

RESULT 12
US-10-243-739-23

```

1      Sequence 23 Application US/10243739
2      Publication No. US20030091593A1
3      GENERAL INFORMATION:
4      APPLICANT: Bachmann, Martin F.
5      APPLICANT: Storn, Razio
6      APPLICANT: Lechner, Franziska
7      TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
8      TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
9      FILE REFERENCE: 1700.0210001
10     CURRENT FILING DATE: 2002-09-16
11     CURRENT FILING DATE: 2002-09-16
12     PRIOR APPLICATION NUMBER: 60/318,967
13     PRIOR FILING DATE: 2001-09-14
14     NUMBER OF SEQ ID NOS: 73
15     SOFTWARE: PatentIn version 3.1
16     SEQ ID NO 23
17     LENGTH: 132
18     TYPE: PRT
19     ORGANISM: Bacteriophage Q-beta
20     US-10-243-739-23

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Query Match	98.8%	Score 655	DB 14	Length 132
Best Local Similarity	98.5%	Pred. No. 3,4e-65		
Matches 130; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0
QY	1	AKLEVTTLGKIGKQKQTLVLP	PRGVNPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK	60
Db	1	AKLEVTTLGKIGRQKQTLVLP	PREVNPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK	60
QY	61	NYKQVAKIQNPACTANGSCDPSV	TRQKADYTFSTQYSTDEERAFAVTELAALLASPL	120
Db	61	NYKQVAKIQNPACTANGSCDPSV	TRQKADYTFSTQYSTDEERAFAVTELAALLASPL	120
QY	121	LIDALDOLNPAY	132	
Db	121	LIDALDOLNPAY	132	

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RESULT 13
US-10-243-739-26
: Sequence 26, Application US/10243739
: Publication No. US20030091593A1
: GENERAL INFORMATION:
: APPLICANT: Bachmann, Martin F.
: APPLICANT: Steornl, Tazio
: APPLICANT: Lecigne, Franziska
: TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of

```

```

? TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
? FILE REFERENCE: 1700. 0210001
? CURRENT APPLICATION NUMBER: US/10/243,739
? CURRENT FILING DATE: 2002-09-16
? PRIOR APPLICATION NUMBER: 60/318,967
? PRIOR FILING DATE: 2001-09-14
? NUMBER OF SEQ. ID NOS.: 73
? SOFTWARE: PatentIn version 3.1
? SEQ. ID NO 26
? LENGTH: 132
? TYPE: PR1
? ORGANISM: Bacteriophage Q-beta
US-10-243-739-26

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Qy	1	AKETVTYIGKIGKQKQTLVLPNGVNPETNGVASISQAGAVPALEKRVTVSVSOPSRRNK	60
Db	1	AKETVTYIGNIGKQKQTLVLPNGVNPETNGVASISQAGAVPALEKRVTVSVSOPSRRNK	60
Qy	61	NYKQVAKIQNTACTANGSCDPSTYTRQKKAADVTSFTQYSTDEBERAFRTIELAALLASPL	120
Db	61	NYKQVAKIQNTACTANGSCDPSTYTRQKKAADVTSFTQYSTDEBERAFRTIELAALLASPL	120
Qy	121	LIDAIIDLQNPAY	132
Db	121	LIDAIIDLQNPAY	132

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RESULT 14
US-10-244-065-23
; Sequence 23, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Weijerink, Edwin
; APPLICANT: Lipowsky, Gerd
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Rehfofs, Regina
; TITLE OR INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; TITLE OF INVENTION: Method of Preparation and Use
; FILE REFERENCE: 1700.022001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-23

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Query March 98.8% Score 655; DB 14 Length 132;
      Local Similarity 98.5%; Pred. NO.3.4e-65;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 AKETVTLIGKIGKQKQTLVLPNGVPTNGSVASISQAGVPALEKRYTVSVSQPSRRRK 60
   |||||
Db 1 AKETVTLIGNIGRQKQTLVLPNGVNPPTNGSVASISQAGVPALEKRYTVSVSQPSRRRK 60
   |||||

QY 61 NYKQVKIQNTACTANGSCDPSYTRQKKAAYVTSFTQYSIDDEEAAPRTIELAALLASPL 120
   |||||

```

```

Query March 98.8% Score 655; DB 14 Length 132;
      Local Similarity 98.5%; Pred. NO.3.4e-65;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 AKETVTLIGKIGKQKQTLVLPNGVPTNGSVASISQAGVPALEKRYTVSVSQPSRRRK 60
   |||||
Db 1 AKETVTLIGNIGRQKQTLVLPNGVNPPTNGSVASISQAGVPALEKRYTVSVSQPSRRRK 60
   |||||

QY 61 NYKQVKIQNTACTANGSCDPSYTRQKKAAYVTSFTQYSIDDEEAAPRTIELAALLASPL 120
   |||||

```

Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIQOLNPAY 132

Db 121 LIDAIQOLNPAY 132

RESULT 15

US-10-244-065-26

; Sequence 26, Application US/10244065

; Publication No. US2003009668A1

; GENERAL INFORMATION:

; APPLICANT: Bachmann, Martin F.

; APPLICANT: Storni, Tazio

; APPLICANT: Maurel, Patrick

; APPLICANT: Tissot, Alain

; APPLICANT: Schwarz, Katrin

; APPLICANT: Meijerink, Edwin

; APPLICANT: Lipowsky, Gerard

; APPLICANT: Pumpens, Paul

; APPLICANT: Clejens, Indulis

; APPLICANT: Renhofa, Regina

; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particl

; FILE REFERENCE: 1700.0220001

; CURRENT APPLICATION NUMBER: US/10/244,065

; PRIOR FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: 60/374,145

; PRIOR FILING DATE: 2002-04-22

; PRIOR APPLICATION NUMBER: 60/318,994

; PRIOR FILING DATE: 2001-09-14

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26

; LENGTH: 132

; TYPE: PR

; ORGANISM: Bacteriophage Q-beta

US-10-244-065-26

Query Match

Best Local Similarity

Matches 130; Conservative

1; Mismatches

1; Indels

0; Gaps

0;

QY 1 ACLEETVLKIGKIDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSQPSRNK 60

Db 1 ACLEETVLKIGKIDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSQPSRNK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDERAFVTEIAALLASPL 120

Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIQOLNPAY 132

Db 121 LIDAIQOLNPAY 132

Search completed: January 4, 2005, 09:41:22

Job time : 33.7351 secs

[illegible][illegible]

A/Residues: 1-529 <RAS>
A/Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PID:CAA42639.1; PID:g44112
A/Experimental source: strain 12067, serotype 4b
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C/Genetics:
A/Gene: hlyA
C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-529/Product: listeriolysin O #status predicted <MAT>

Query Match 12.7% Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.1;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGGKOTLVL-----NPRGVNPTNGVASISQGA-----VPALERKV 48
DB 93 KDGENEYIVVEKKKKSINQNMADIQVNAISSITFGALVKANSELVENQPDVLPYKRBSL 152
QY 49 TVSVSQPSRNKNYQVQKIQNPACTANGSCDPSVTR-----QKVDVTFSSFTQYSTD 102
DB 153 TLTSIDLPGMTQDNKIIVK--NATKSNVNNNAVTLVERNKEKYAQAYPNVS---AKIDYD 207
QY 103 EERAFVETELAA 114
DB 208 DEMAYSESOLIA 219

RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C/Species: Listeria monocytogenes
C/Date: 21-Oct-1992 #sequence revision 21-Oct-1992 #text_change 09-Jul-2004
C/Accession: A43505; S05306; A47606; S12400; A61079
R/Mengaud, J.; Vicente, M.F.; Chenerey, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanrey
Infect. Immun. 56, 766-772, 1988
A/Title: Expression in Escherichia coli and sequence analysis of the listeriolysin O de
A/Reference number: A43505; MUID:88153053; PMID:3126142
A/Accession: A43505
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <MEN>
A/Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PID:AAA03018.1; PID:g149653
A/Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R/Dommann, R.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A/Title: Nucleotide sequence of the listeriolysin gene from a Listeria monocytogenes ser
A/Reference number: S05306; MUID:89366684; PMID:2505236
A/Accession: S05306
A/Molecule type: DNA
A/Residues: 1-529 <DOM>
A/Cross-references: EMBL:X15127; NID:g44106; PID:CAA33223.1; PID:g44107
A/Experimental source: strain EGD from a weakly hemolytic strain, serotype 1/2a
R/Mengaud, J.; Chenerey, J.; Geoffroy, C.; Galliard, J.L.; Cosset, P.
Infect. Immun. 55, 3225-3227, 1987
A/Title: Identification of the structural gene encoding the SH-activated hemolysin of Li
A/Reference number: A47606; MUID:88057627; PMID:2824384
A/Accession: A47606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 413-480 <ME2>
A/Cross-references: GB:M29171
R/Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cosset, P.
Mol. Microbiol. 4, 2167-2178, 1990
A/Title: Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtain
A/Reference number: S12400; MUID:91211627; PMID:1965218
A/Accession: S12400
A/Molecule type: DNA
A/Residues: 483-493 <MIC>
A/Experimental source: strain L028, serotype 1/2c
C/Genetics:
A/Gene: hlyA; hlyB

C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-529/Product: listeriolysin O #status predicted <MAT>

Query Match 12.7% Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.1;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGGKOTLVL-----NPRGVNPTNGVASISQGA-----VPALERKV 48
DB 93 KDGENEYIVVEKKKKSINQNMADIQVNAISSITFGALVKANSELVENQPDVLPYKRBSL 152
QY 49 TVSVSQPSRNKNYQVQKIQNPACTANGSCDPSVTR-----QKVDVTFSSFTQYSTD 102
DB 153 TLTSIDLPGMTQDNKIIVK--NATKSNVNNNAVTLVERNKEKYAQAYPNVS---AKIDYD 207
QY 103 EERAFVETELAA 114
DB 208 DEMAYSESOLIA 219

RESULT 8
AC1100
Listeriolysin O precursor [Imported] - Listeria monocytogenes (strain EGD-e)
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC1100
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baghero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Falhi, H.;
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schuster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1100
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <GLA>
A/Cross-references: UNIPROT:P13128; GB:NC_003210; PID:CAD00729.1; PID:g16409567; GSPDB:C
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: hly
C/Superfamily: dipeptide transport protein

Query Match 12.7% Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.1;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGGKOTLVL-----NPRGVNPTNGVASISQGA-----VPALERKV 48
DB 93 KDGENEYIVVEKKKKSINQNMADIQVNAISSITFGALVKANSELVENQPDVLPYKRBSL 152
QY 49 TVSVSQPSRNKNYQVQKIQNPACTANGSCDPSVTR-----QKVDVTFSSFTQYSTD 102
DB 153 TLTSIDLPGMTQDNKIIVK--NATKSNVNNNAVTLVERNKEKYAQAYPNVS---AKIDYD 207
QY 103 EERAFVETELAA 114
DB 208 DEMAYSESOLIA 219

RESULT 9
T31660
Hypothetical protein COS41.6 - sea squirt (Cliona intestinalis)
C/Species: Cliona intestinalis
C/Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T31660
R/Bird, A.P.; Clark, V.; Jones, S.J.; Letigeb, S.; Dobson, R.; Tweedle, S.
submitted to the EMBL Data Library, December 1996
A/Reference number: Z21049
A/Accession: T31660

A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-432 <BIR>
 A:Cross-references: UNIPROT:P1584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDD:CA06065
 A:introns: 180/2; 212/1; 229/3

Query Match 12.2%; Score 81; DB 2; Length 432;
 Best Local Similarity 28.3%; Pred. No. 3.7;
 Matches 32; Conservative 17; Mismatches 46; Indels 18; Gaps 6;

QY 4 EYVTLKIGKDGKQTLVLPNGVNPNGVSLGQAGVPALEKRVTVSVSQPSRKRKTK 63
 DB 242 DTSSEGEVLTKDGGNLAENP---TPSNAARELOESVASEVLETVVKSALIQ-EQDSAAVR 297
 QY 64 VQVKIONPAPAC-TANGSC-----DPSVTRCKYAD-----VTFSTQYSTDE 103
 DB 298 KR-NPONAPACPNRNGNCVSTNSNKTNDKRIEIVNSDDNTDEDTQIDTNE 349

RESULT 10
 S22341
 Ivanolysin precursor - Listeria ivanovii
 C:Species: Listeria ivanovii
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C:Accession: S22341; S36683
 R:Haas, A.; Dumbeky, M.; Krefl, J.
 Biochim. Biophys. Acta 1130, 81-84, 1992
 A:Title: Listeriolysin genes: complete sequence of 110 from Listeria ivanovii and of 1ac
 A:Reference number: S22340; M01D:92182018; PMID:1543752
 A:Accession: S22341
 A:Molecule type: DNA
 A:Residues: 1-528 <HMS>
 A:Cross-references: UNIPROT:P1831; EMBL:X60461
 A:Note: the authors translated the codon ACA for residue 331 as Val
 R:Krefl, J.
 submitted to the EMBL Data Library, July 1991
 A:Reference number: S36683
 A:Accession: S36683
 A:Molecule type: DNA
 A:Residues: 1-319, 'T', 321-528 <KR>
 A:Cross-references: EMBL:X60461
 C:Genetics: 110
 A:Gene: 110
 C:Superfamily: dipeptide transport protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:35-528/Product: Ivanolysin #status predicted <MAT>

Query Match 12.1%; Score 80.5; DB 2; Length 528;
 Best Local Similarity 22.0%; Pred. No. 5.3;
 Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDKGKQLVL-----NRGVNPTNGVSLGQAG-----VPALEKRY 48
 DB 92 KEENQYIVAEKKKKSINQNNADIQVINSLSLTPGALVANSSELVENQPDVLPVKRDSV 151
 QY 49 TVSVQPSRRKRYKVKVQKIQNPACTANGSCDPSVTR-----QKADVTFFSTQYSTD 102
 DB 152 TLEIDLP--GMVNDHNEIVQVQNTKSNINDGVNTLVDRMNNKXSEETPNIS---AKIDYD 206
 QY 103 EERAFVTELA 114
 DB 207 QEMAYSESQVVA 218

RESULT 11
 RGBH1
 CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein 1672.1; protein YLR256w; regulatory protein CYP1; regulatory
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1991 #sequence_revision 23-Feb-1996 #text_change 12-Nov-1999
 C:Accession: S59400; A31312; S15447; S05804; S15446
 R:Johnson, D.

submitted to the EMBL Data Library, February 1995
 A:Description: The sequence of S. cerevisiae cosmid 9672.

A:Reference number: S59386
 A:Accession: S59400
 A:Molecule type: DNA
 A:Residues: 1-1502 <JCH>
 A:Cross-references: EMBL:U20865; NID:g662330; PIDD:AA67387.1; PID:g662331; GSPDB:GN0001;
 A:Experimental source: strain S288C (AB972)
 R:Pfeiffer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
 Cell 56, 291-301, 1989

A:Title: Functional dissection and sequence of yeast HAP1 activator.
 A:Reference number: A31312; M01D:89106221; PMID:2643482
 A:Accession: A31312
 A:Molecule type: DNA
 A:Residues: 1-144, 'T', 146-322, 'R', 324-454, 'N', 456-507, 'W', 509-586, 'K', 588-882, 'N', 884-95;
 A:Cross-references: EMBL:U03152; NID:g171645; PIDD:AAA34662.1; PID:g171646
 R:Creusot, F.; Verdier, J.; Galene, M.; Slonimski, P.P.
 U. Mol. Biol. 204, 263-276, 1988

A:Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
 A:Reference number: S15447; M01D:89125585; PMID:2851558
 A:Accession: S15447
 A:Molecule type: DNA
 A:Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPIME' <CRE1>
 A:Cross-references: EMBL:X13793
 A:Note: the sequence is from mutant CYP1-18
 C:Genetics: 18
 A:Gene: SGD:HAP1; CYP1; MIPS:YLR256w
 A:Cross-references: SGD:S0004246; MIPS:YLR256w

A:Map position: 12R
 C:Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology
 C:Keywords: DNA binding; heme binding; transcription regulation; zinc finger
 F:1-148/Domain: DNA binding #status predicted <DNA>
 F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:64-84/Region: zinc finger CCCC motif
 F:177-189/Region: glutamine-rich
 F:245-445/Domain: heme binding #status predicted <HEM>
 F:299-304, 323-328, 347-352, 373-378, 388-394, 415-420/Region: 6-residue repeats
 F:1308-1481/Domain: activation element #status predicted <ACT>
 F:1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
 Best Local Similarity 20.6%; Pred. No. 16;
 Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;

QY 23 PRGVN--PTNGVASL-----SQAGVPALEKRVTVSVS 53
 DB 1278 PRGISPKPENGSSVGPPLISSFSMNQNGTTPVPSLNTTSQWALPSLDRITNQIN 1337
 QY 54 QPSRNR-KNYKQVQKIQNP-----TACTANGSCP 82
 DB 1338 LPDPSDEAFDMSIKOMTPWTSAPNNANTTIPSTINGMNNMGAGTANTDTSANGSALS 1397
 QY 83 SVTRCKYADV-TFSFTQYSTD--EERAFVTELAALASP-TLIDALDQIN 129
 DB 1398 TLTSFGSGLASNSATQKPDLEDFLMQNSFNGLMINSLSLVEVVGIN 1447

RESULT 12
 C98221
 hypothetical protein AGR_L1428 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: C98221
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappae, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; M01D:21608551; PMID:11743194
 A:Accession: C98221
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KUR>
 A:Cross-references: UNIPROT:Q8U8F3; GB:AE007870; PIDD:AAK89293.1; PID:g15159127; GSPDB:GN

C:Genetics:
A:Gene: AGR_L1428
A:Map position: linear chromosome

Query Match 12.0%; Score 79.5; DB 2; Length 136;
Best Local Similarity 25.4%; Pred. No. 1.4;
Matches 30; Conservative 15; Mismatches 56; Indels 17; Gaps 3;

Qy 11 IGDGKQTLVLPNGVNPFGVSLQAGAV-----PALEKRVTSVSGPSRRR 59
Db 3 ISKDKQTESADPHMIEMVTGTISTLVAMFGWIAVDYRYSPEBARFEIANTGVGEQT 62

Qy 60 KNYKVQVXIONFTACTA-----NGSCDPSVTRQKADVTFSF-TQYSTDEBARFVTE 111
Db 63 GQYRVKFAIHNLSMTTAAQVNVGRDLEQNGASPENADVTFDYVASESKDNGTLFFRSD 120

RESULT 13
A:Accession: AE3065
conserved hypothetical protein Atu4139 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE3065
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyaev, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3065
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q8UAR3; GB:AE0086689; PIDD:AL44939.1; PID:g17742593; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4139
A:Map position: linear chromosome

Query Match 12.0%; Score 79.5; DB 2; Length 136;
Best Local Similarity 25.4%; Pred. No. 1.4;
Matches 30; Conservative 15; Mismatches 56; Indels 17; Gaps 3;

Qy 11 IGDGKQTLVLPNGVNPFGVSLQAGAV-----PALEKRVTSVSGPSRRR 59
Db 3 ISKDKQTESADPHMIEMVTGTISTLVAMFGWIAVDYRYSPEBARFEIANTGVGEQT 62

Qy 60 KNYKVQVXIONFTACTA-----NGSCDPSVTRQKADVTFSF-TQYSTDEBARFVTE 111
Db 63 GQYRVKFAIHNLSMTTAAQVNVGRDLEQNGASPENADVTFDYVASESKDNGTLFFRSD 120

RESULT 14
A:Accession: A10186
Probable iron-siderophore transport system, ATP-binding component YPO1533 [imported] - Y
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: A10186
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
11, M.; Rutherford, K.; Stimmendorf, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10186
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <KUR>
A:Cross-references: UNIPROT:Q8ZFZ0; GB:AL590842; PIDD:CAK90356.1; PID:g15979576; GSPDB:C
C:Genetics:
A:Gene: YPO1533

C:Superfamily: inner membrane protein malk; ATP-binding cassette homology

Query Match 11.9%; Score 79; DB 2; Length 282;
Best Local Similarity 22.0%; Pred. No. 3.6;
Matches 27; Conservative 37; Mismatches 45; Indels 14; Gaps 5;

Qy 13 KQKQTLVLPNGVNPFGVSLQAGAVPALEKRVTSVSGPSRRRKNYKVQVXIONFT 72
Db 49 KNGAFSVIIGPNCCKSTLRALSRS---LLPONGSIRLDQ--QDIQYKAKVFARQLS 102

Qy 73 ACTANGSCDPSVT-----ROKADVTFSFTQYSTDEBARFVTEALALASPLIDAID 126
Db 103 LLSQASISSETITVDVYSRGRYHQSF-FHQMSIEDER-IYKALISAVNLESIVQGRVS 160

Qy 127 QLN 129
Db 161 ELS 163

RESULT 15
H90078
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90078
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9756; MUID:21311952; PMID:11418146
A:Accession: H90078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <KUR>
A:Cross-references: UNIPROT:Q99QUS; GB:BA000018; PIDD:g13702654; PIDD:BA843794.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2488

Query Match 11.8%; Score 78.5; DB 2; Length 191;
Best Local Similarity 24.1%; Pred. No. 2.6;
Matches 27; Conservative 24; Mismatches 50; Indels 11; Gaps 3;

Qy 6 VTLGKIGKQTLVLPNGVNPFGVSLQAGAV-----GAVPALEKRVTSVSGPSRRR 59
Db 1 MTLPRKIGKPA--TRALNQGITYTLEAVSQYTKSSLMENHGVGP---KAISILEQALFQHQ 55

Qy 60 KNYKVQVXIONFTACTANGSCDPSVTRQKADVTFSF-TQYSTDEBARFVTE 111
Db 56 LHFKEVQSLPFLKLTGVSCVHAPKQOMIDFIVATALDIELRLSVTTE 107

Search completed: January 4, 2005, 09:17:30
Job time : 9.03224 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-7
Perfect score: 663
Sequence: 1 AKLEYTLGKIGKDGKQTLV.....AALIASPLIDAIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_02:*\n uniprot_sprot:*\n 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.3	133	1	COAT_BPOBE
2	652	98.3	133	2	AAM33126
3	652	98.3	329	2	08LNEI
4	652	98.3	329	2	AAL16663
5	565	85.2	133	2	09TOR9
6	565	85.2	329	2	064307
7	545	82.2	133	2	09TOS0
8	545	82.2	329	2	064303
9	537.5	81.1	132	1	COAT_BPSP
10	537.5	81.1	331	1	VAI_BPSP
11	497.5	75.0	132	2	09TOR8
12	497.5	75.0	330	2	064310
13	116	17.5	131	1	COAT_BPPRR
14	93	14.0	473	1	08VDC2
15	90.5	13.7	530	1	TACY_LISSE
16	90.5	13.7	530	2	AAP97361
17	88.5	13.3	540	2	048683
18	84.5	12.7	529	1	TACY_LISMF
19	84.5	12.7	529	1	TACY_LISMO
20	84.5	12.7	529	2	09L5B9
21	84.5	12.7	529	2	06B942
22	84.5	12.7	529	2	06B9A2
23	84.5	12.7	529	2	06B9G2
24	84.5	12.7	529	2	06B9Q2
25	84.5	12.7	529	2	06B9T2
26	84.5	12.7	529	2	06B9A28
27	84.5	12.7	529	2	06B9A6
28	84.5	12.7	529	2	06B9AB7
29	84.5	12.7	529	2	06B9AB0
30	84.5	12.7	529	2	06B9AD4
31	84.5	12.7	529	2	AAT03000

32	84	12.7	1624	2	Q9V3K8	Q9V3K8 drosophila
33	84	12.7	1637	2	Q9SRU8	Q9SRU8 drosophila
34	82.5	12.4	461	2	Q7PP73	Q7PP73 anopheles g
35	82	12.4	336	2	Q8RRP3	Q8RRP3 methanosarc
36	82	12.4	512	2	Q6HGA7	Q6HGA7 bacillus th
37	81.5	12.3	608	2	Q84H79	Q84H79 rhodococcus
38	81	12.2	432	2	P91584	P91584 clostridia
39	80.5	12.1	528	1	TACY_LISIV	P31831 listeria iv
40	80.5	12.1	528	2	Q6R6D9	Q6R6D9 listeria iv
41	80.5	12.1	528	2	AAR97343	AAR97343 listeria
42	80.5	12.1	1502	1	CYPI_YEAST	P12351 saccharomyc
43	79.5	12.0	136	2	Q7CU57	Q7CU57 agrobacteri
44	79.5	12.0	136	2	Q8U8F3	Q8U8F3 agrobacteri
45	79	11.9	282	2	Q8ZFZ0	Q8ZFZ0 yersinia pe

ALIGNMENTS

RESULT 1
ID COAT_BPOBE STANDARD; PRT; 132 AA.
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirgatus.
OX NCBI_Taxid=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Dreilima D., Dieters A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmis C., Sastry P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
RT bacteriophage Q-beta as an application of a mapping procedure for RNA
RT fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=818709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
RT and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiz T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Valergard K., Liljas L.;
RT "The crystal structure of Bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M99039; AAA16662.1; --

DR EMBL; V00643; CAA23992.1; --

DR PIR; A92240; VCBPOB.

DR PDB; 1QBE; X-ray; A/B/C=1-132.

DR InterPro; IPR002703; Lev1_coat.

DR 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.

KM Pfam; PF01819; Lev1_coat; 1.

FT INIT MET 0 0

FT CONFLICT 22 22 N -> D (in Ref. 4).

FT CONFLICT 56 56 Missing (in Ref. 4).

FT STRAND 6 9

FT TURN 13 14

FT STRAND 18 27

FT TURN 28 31

FT STRAND 32 36

FT STRAND 42 44

FT HELIX 47 53

FT STRAND 56 58

FT TURN 57 58

FT STRAND 59 59

FT STRAND 62 74

FT STRAND 83 96

FT TURN 98 99

FT HELIX 102 117

FT HELIX 119 126

FT TURN 127 127

SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.3%; Score 652; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 2,4e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKETVTTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSPSRNRK 60
DB 1 AKETVTTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSPSRNRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTIELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTIELAALLASPL 120

QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 2
AAM33126 PRELIMINARY; PRT; 133 AA.

ID AAM33126
AC AAM33126;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviriviruses; Alloviriviruses subgroup III.
OK NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."; BMC Evol. Biol. 3:24-24(2003).
DR EMBL; AY099114; AAM33126.1; --
KW Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.3%; Score 652; DB 2; Length 133;
Best Local Similarity 98.5%; Pred. No. 2,4e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKETVTTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSPSRNRK 60
DB 2 AKETVTTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSPSRNRK 61

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTIELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTIELAALLASPL 121

QY 121 LIDAIQDLPAY 132
DB 122 LIDAIQDLPAY 133

RESULT 3
Q8LTEL PRELIMINARY; PRT; 329 AA.

ID Q8LTEL
AC Q8LTEL;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviriviruses.
OK NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."; BMC Evol. Biol. 3:24-24(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanis V., Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; AY099114; AAM33127.1; --
DR EMBL; M99039; AAA16663.1; --
DR HSP; P03615; 1QBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.3%; Score 652; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 7e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKETVTTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSPSRNRK 60
DB 2 AKETVTTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSPSRNRK 61

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTIELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTIELAALLASPL 121

QY 121 LIDAIQDLPAY 132
DB 122 LIDAIQDLPAY 133

RESULT 4
AAA16663 PRELIMINARY; PRT; 329 AA.

ID AAA16663
AC AAA16663;
DT 02-MAR-2004 (TREMBlrel. 27, Created)

DT 02-MAR-2004 (TRENBLREL. 27, last sequence update)
DT 02-MAR-2004 (TRENBLREL. 27, last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
NCBI_TaxId=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielens I., Drellina D., Dielera A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; M99039; AAA16663.1; -
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;
SO

Query Match 98.3%; Score 652; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 7e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYLGKIGDKQKQTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSOPSRRNK 61

QY 61 NKVVQVKIONPTACTANGSCDPSVTRQKADYVTFSTQYSTDERRAFVTELAALASPL 120
DB 62 NKVVQVKIONPTACTANGSCDPSVTRQKADYVTFSTQYSTDERRAFVTELAALASPL 121

QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
ID Q9TOR9;
AC Q9TOR9;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
NCBI_TaxId=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14699.1; -
DR HSSP; P03615; 10BE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coa protein.
SQ SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;
SO

Query Match 85.2%; Score 565; DB 2; Length 133;
Best Local Similarity 83.3%; Pred. No. 6.9e-47;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYLGKIGDKQKQTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSOPSRRNK 61

QY 61 NKVVQVKIONPTACTANGSCDPSVTRQKADYVTFSTQYSTDERRAFVTELAALASPL 120
DB 62 NKVVQVKIONPTACTANGSCDPSVTRQKADYVTFSTQYSTDERRAFVTELAALADPM 121

QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TRENBLREL. 07, Created)
DT 01-AUG-1998 (TRENBLREL. 07, last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
NCBI_TaxId=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14700.1; -
DR HSSP; P03615; 10BE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;
SO

Query Match 85.2%; Score 565; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 2e-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYLGKIGDKQKQTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSOPSRRNK 61

QY 61 NKVVQVKIONPTACTANGSCDPSVTRQKADYVTFSTQYSTDERRAFVTELAALASPL 120
DB 62 NKVVQVKIONPTACTANGSCDPSVTRQKADYVTFSTQYSTDERRAFVTELAALADPM 121

QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

```

RESULT 7
ID Q9T0S0 PRELIMINARY; PRT; 133 AA.
AC Q9T0S0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Coat protein. M11.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
OX NCBI_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coat protein.
KM
SQ SEQUENCE 133 AA; 14198 MW; 098722E3C6CA255 CRC64;

Query Match 82.2%; Score 545; DB 2; Length 133;
Best Local Similarity 80.3%; Pred. No. 6e-45;
Matches 106; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 AKLETYTLGKIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLQATLTLGKIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LVNAIDINLPAY 133

RESULT 8
ID Q64303 PRELIMINARY; PRT; 329 AA.
AC Q64303;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
OX NCBI_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06251.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35893 MW; 3B33CDB21EE625F4 CRC64;

Query Match 82.2%; Score 545; DB 2; Length 329;
Best Local Similarity 80.3%; Pred. No. 1.7e-44;
Matches 106; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 AKLETYTLGKIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLQATLTLGKIGKDGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LVNAIDINLPAY 133

RESULT 9
ID COAT_BPSP STANDARD; PRT; 132 AA.
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
OX NCBI_TaxID=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; X07489; CAA0374.1; -.
DR HSSP; P03615; IQBE.

```

DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat; 1.
 KW Coat protein; RNA-binding.
 SQ SEQUENCE 132 AA; 14129 MW; 50B1E6CC6A0A254 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 132;
 Best Local Similarity 79.5%; Pred. No. 3.2e-44;
 Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLETTTLGKIGDKGQTLVLPNGVNPPTNGVSLSOAGAVPALBKRVTVSQPSRNRK 60
 DB 2 AKLNQVTLKIGKNGGQTLTLTPRGVNPPTNGVSLSEAGAVPALBKRVTVSQPSRNRK 61
 QY 61 NYKVQVKTIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDERRAFVTELAALASP 120
 DB 62 NFKVQIKLONPACTRD-ACDPSVTRSAFADVTLSFTSYSTDERRALIRTELAALADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IYDAIDNINPAY 132

RESULT 10
 VAL_BPSP STANDARD; PRT; 331 AA.
 AC P09677;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Readthrough protein A1 [contains: Coat protein].
 OS Bacteriophage SP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allolevivirus.
 OX NCBI_Taxid=12027;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289362; PubMed=3399390;
 RA Hirashina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
 RT "Analysis of the complete nucleotide sequence of the group IV RNA
 RT coliphage SP."
 RL Nucleic Acids Res. 16:6205-6221(1988).
 CC -1- FUNCTION: Not yet known.
 CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
 CC protein sequence.

CC -----
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 CC -----
 CC EMBL; X07489; CAB37299.1; -.
 DR PIR; S01964; S01964.
 DR HSSP; P03615; 10BE.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat; 1.
 KW Coat protein.
 FT CHAIN 1 132 Coat protein.
 FT CHAIN 1 331 Readthrough protein A1.
 SQ SEQUENCE 331 AA; 36203 MW; 4A6642E4B52C6582 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 331;
 Best Local Similarity 79.5%; Pred. No. 9.2e-44;
 Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLETTTLGKIGDKGQTLVLPNGVNPPTNGVSLSOAGAVPALBKRVTVSQPSRNRK 60
 DB 2 AKLNQVTLKIGKNGGQTLTLTPRGVNPPTNGVSLSEAGAVPALBKRVTVSQPSRNRK 61
 QY 61 NYKVQVKTIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDERRAFVTELAALASP 120
 DB 121 IYDAIDNINPAY 132

DB 62 NFKVQIKLONPACTRD-ACDPSVTRSAFADVTLSFTSYSTDERRALIRTELAALADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IYDAIDNINPAY 132

RESULT 11
 O9TOR8 PRELIMINARY; PRT; 132 AA.
 ID O9TOR8
 AC O9TOR8;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allolevivirus.
 OX NCBI_Taxid=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RT RNA phage Q beta."
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis."
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14703.1; -.
 DR HSSP; P03615; 10BE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat; 1.
 KW Coat protein.
 SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 75.0%; Score 497.5; DB 2; Length 132;
 Best Local Similarity 75.8%; Pred. No. 2.4e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLETTTLGKIGDKGQTLVLPNGVNPPTNGVSLSOAGAVPALBKRVTVSQPSRNRK 60
 DB 2 AKLNQVTLKIGKNGGQTLTLTPRGVNPPTNGVSLSEAGAVPALBKRVTVSQPSRNRK 61
 QY 61 NYKVQVKTIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDERRAFVTELAALASP 120
 DB 62 NFKVQIKLONPACTRD-ACDPSVTRSGSDVTLSFTSYSTDERRALIRTELAALADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IYDAIDNINPAY 132

RESULT 12
 O64310 PRELIMINARY; PRT; 330 AA.
 ID O64310
 AC O64310;
 DT 01-AUG-1998 (TRENBLREL. 07, Created)
 DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Al-protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC A10Levivirus.
 OX NCBI_TaxID=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta."
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Post R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; A014704.1; -.
 DR HSP; P03615; 10BE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Levi coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 DR SEQUENCE 330 AA; 36175 MW; 961E55F408334410 CRC64;
 SQ
 Query Match 75.0%; Score 497.5; DB 2; Length 330;
 Best Local Similarity 75.8%; Pred. No. 7,1e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKETVTGKIGKDGKQTLVNPGRVPTNGVSLGAGVPALEKRVTVSVQPSNRK 60
 DB 2 AKLNKVLITGIGKAGNGLTLTPRGVPTNGVSLGAGVPALEKRVTVSVQPSNRK 61
 QY 61 NYKQVQIOPNPTACTANGSCDPSVTRQKVDVTFSPQYSTDEERAFVTELAALASPL 120
 DB 62 NYKQVQIKQNPACTCKO-ACDPSVTRSGSRDVTLSFTSYSTERRALIRTELAKDL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADINLNPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR STANDARD; PRT; 131 AA.
 AC P03615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhasee P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell, binds to the phage RNA.
 DR InterPro; IPR002703; Levi coat.
 DR Pfam; PF01819; Levi coat; 1.
 KW Coat protein; direct protein sequencing; RNA-binding;
 SQ SEQUENCE 131 AA; 14535 MW; E7E639E1B50FC612 CRC64;

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0027;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTLVNPGRVPTNGVSLGAGVPALEKRVTVSVQPSNRKRYKVQV 66
 DB 4 QNLVVKDREATPNHDTFVPRDIRDVNGEVSTGVPIESRPTISLRRTSNGR--YKSTL 61
 QY 67 KIQNPT--ACTANGSCDPSVTRQKVDVTFSPQYSTDEER-AFVTELAALASPLLI- 122
 DB 62 KLVFVWQSQTIVANGIVTVFVTVTSYTVDFDYDASTKERNNFGMTADAKDLMLVH 121
 QY 123 DAIDQINPAY 132
 DB 122 DTLVNLQGVY 131
 RESULT 14
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Tmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darat E., Kiss C., Kost-Alimova M., Klein G., Dumanaki J.P.,
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3."
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL; AJ248064; CAD20986.1; -.
 DR MGD; MGI:2446841; Tmem7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0E69F2A4D CRC64;
 Query Match 14.0%; Score 93; DB 2; Length 473;
 Best Local Similarity 26.1%; Pred. No. 2;
 Matches 40; Conservative 17; Mismatches 34; Indels 62; Gaps 6;
 QY 22 NPGVNPNG---VASLSQAGAVP-----ALEKRVTVSVQPSNRKRYKVQV---- 66
 DB 219 NPGASNPTKNDPDKVSCTSKRPAPLSPSTLSKARBEKRVTVCSNISRSSSKVQMPQAS 278
 QY 67 ----KIQNPT-----ACTANGSCDPSVTRQ-----KX 89
 DB 279 KNPQTSNPDKNDPKISTCSKSTYRLTLTQLSVSPAPAPTCVQMPSPPIIDGSA 338
 QY 90 ADVTFSTQYSTDEERAFVTELAALASPLLI 122
 DB 339 ADVAKENTRSKTPK-----ALLSSPLIV 361
 RESULT 15
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeryolysin precursor (Thiol-activated cytolysin).
 GN Name=Isol;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-6

Perfect score: 664
Sequence: 1 ALEFVTLGIGNRDQKTLV.....AALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	664	100.0	132 5	ABG94316
2	664	100.0	132 5	ABG80628 Bacteriop
3	664	100.0	132 6	ABR56452
4	664	100.0	132 6	ABU09689 Bacteriop
5	664	100.0	132 6	ABR44555 Bacteriop
6	664	100.0	132 7	ADD24130 Bacteriop
7	664	100.0	132 7	ADJ82056 Protein f
8	664	100.0	132 7	ADK17144 Virus-11k
9	664	100.0	132 8	ADJ36313 Bacteriop
10	664	100.0	132 8	ADJ67159 Phage Qbe
11	664	100.0	132 8	ADK52193 Bacteriop
12	661	99.5	132 5	ABG94318
13	661	99.5	132 5	ABG80630 Bacteriop
14	661	99.5	132 6	ABR56454 Bacteriop
15	661	99.5	132 6	ABU09691 Bacteriop
16	661	99.5	132 6	ABR44557 Bacteriop
17	661	99.5	132 7	ADD24132 Bacteriop
18	661	99.5	132 7	ADJ82058 Protein f
19	661	99.5	132 7	ADK17146 Virus-11k
20	661	99.5	132 8	ADJ36315 Bacteriop
21	661	99.5	132 8	ADJ67161 Phage Qbe
22	661	99.5	132 8	ADK52195 Bacteriop
23	658	99.1	132 5	ABG94320 POB251 pr
24	658	99.1	132 5	ABG80632 Bacteriop
25	658	99.1	132 6	ABR56455 Bacteriop

26	658	99.1	132 6	ABU09693 Bacteriop
27	658	99.1	132 6	ABR44558 Bacteriop
28	658	99.1	132 7	ADD24133 Bacteriop
29	658	99.1	132 7	ADJ82059 Protein f
30	658	99.1	132 7	ADK17147 Virus-11k
31	658	99.1	132 8	ADJ36316 Bacteriop
32	658	99.1	132 8	ADJ67162 Phage Qbe
33	658	99.1	132 8	ADK52196 Bacteriop
34	655	98.6	132 5	ABG94233 Bacteriop
35	655	98.6	132 5	ABG94317 POB243 pr
36	655	98.6	132 5	ABG94319 POB259 pr
37	655	98.6	132 5	ABG80629 Bacteriop
38	655	98.6	132 5	ABG80631 Bacteriop
39	655	98.6	132 5	ABG80545 Bacteriop
40	655	98.6	132 5	ABR56456 Bacteriop
41	655	98.6	132 6	ABR56439 Bacteriop
42	655	98.6	132 6	ABR56453 Bacteriop
43	655	98.6	132 6	ABU09686 Bacteriop
44	655	98.6	132 6	ABU09690 Bacteriop
45	655	98.6	132 6	ABU09692 Bacteriop

ALIGNMENTS

RESULT 1	
ABG94316	
ID	ABG94316 standard; protein; 132 AA.
XX	
AC	ABG94316;
XX	
DT	29-AUG-2003 (revised)
DT	10-DEC-2002 (first entry)
XX	
DE	POB240 protein.
XX	
KW	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW	cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW	vaccine; infectious disease.
XX	
OS	unidentified bacteriophage.
XX	
PN	WO200256905-A2.
XX	
PD	25-JUL-2002.
XX	
PF	21-JAN-2002; 2002WC-IB000166.
XX	
PR	19-JAN-2001; 2001US-0262379P.
PR	04-MAY-2001; 2001US-0288549P.
PR	05-OCT-2001; 2001US-0326988P.
PR	07-NOV-2001; 2001US-0331045P.
XX	
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.
PI	Renner WA, Bachmann M, Tiesot A, Maurer P, Lechner F, Sebbel P;
PI	Pioseck C;
XX	
DR	WPI; 2002-627351/67.
XX	
PT	Molecular antigen array used in the production of vaccines for infectious
PT	diseases.
XX	
PS	Claim 18; Page 144; 441pp; English.
XX	
CC	This invention relates to a novel ordered and repetitive antigen array
CC	used in the production of vaccines for infectious diseases. The invention
CC	also discloses a composition comprising a non-natural molecular scaffold
CC	comprising a core particle selected from a core particle of a non-natural
CC	origin and a core particle of natural origin and an organiser comprising
CC	at least one first attachment site, where the organiser is connected to
CC	the core particle by at least one covalent bond. Also disclosed is an
CC	antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abetal-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1e-70; Indels 0; Gaps 0;
 Matches 132; Conservative 0; Mismatches 0;

Qy 1 AKLETVTLGNIGRGKQTLVLRGNVPPTNGVASTLSQAGVAPLAEKRVTVSOPSRRNK 60
 Db 1 AKLETVTLGNIGRGKQTLVLRGNVPPTNGVASTLSQAGVAPLAEKRVTVSOPSRRNK 60

Qy 61 NYKVQVKIQNPPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETLAALLASPL 120
 Db 61 NYKVQVKIQNPPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETLAALLASPL 120

Qy 121 LIDAIQDLNPAY 132
 Db 121 LIDAIQDLNPAY 132

RESULT 2

ABG80628 standard; protein; 132 AA.

29-NOV-2002 (first entry)

Bacteriophage Q-beta A1 coat protein mutant Qbeta-240.

CC Molecular antigen array; vaccine; antigen; antimicrobial;
 CC molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 CC graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 CC adult respiratory distress syndrome; ARDS; Crohn's disease;
 CC allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 CC Grave's disease; systemic lupus erythematosus; osteoporosis;
 CC inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 CC immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 CC angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 CC rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 CC enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.

OS Synthetic.

PN W0200256907-A2.

25-JUL-2002.

21-JAN-2002; 2002WO-1B000168.

19-JAN-2001; 2001US-0262379P.

04-MAY-2001; 2001US-0286549P.
 PR 05-OCT-2001; 2001US-0326989P.
 PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVA) NOVARTIS PHARMA AG.

PA (MAUR/) MAUSER P.

PA (LECH/) LECHNER F.

PA (ORTM/) ORTMANN R.

PA (LUEB/) LUEBEND R.

PA (STAU/) STAUDENBIEL M.

PA (FREY/) FREY P.

PI Maurer P, Lechner F, Ortmann R, Luegend R, Staudenbiel M, Frey P;

PI Renner WA, Bachmann M, Tissot A, Seibel P, Plosek C;

XX MPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

XX Example 18; Page 144; 418pp; English.

CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

SO Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1e-70; Indels 0; Gaps 0;
 Matches 132; Conservative 0; Mismatches 0;

Qy 1 AKLETVTLGNIGRGKQTLVLRGNVPPTNGVASTLSQAGVAPLAEKRVTVSOPSRRNK 60

Db 1 AKLETVTLGNIGRGKQTLVLRGNVPPTNGVASTLSQAGVAPLAEKRVTVSOPSRRNK 60

Qy 61 NYKVQVKIQNPPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETLAALLASPL 120

Db 61 NYKVQVKIQNPPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVRETLAALLASPL 120

Qy 121 LIDAIQDLNPAY 132

Db 121 LIDAIQDLNPAY 132

RESULT 3

ABR56452 standard; protein; 132 AA.

XX ABR56452;
AC
XX
DT 28-JUL-2003 (first entry)
XX
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:23.
XX

Antigen presenting cell, APC; immune response; virus like particle, VLP;
KM cytotoxic; virucide; antibacterial; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KM antihypertensive; antidiabetic; neuroprotective; nootropic; osteoprotic;
KM antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.

XX Bacteriophage Qbeta.
OS Synthetic.
XX WO2003024480-A2.
XX

XX 27-MAR-2003.
XX

XX 16-SEP-2002; 2002WO-IB004252.
XX

XX 14-SEP-2001; 2001US-0318967P.
XX

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX

XX Bachmann M, Storni T, Lechner F;
XX

XX WPI; 2003-363095/34.
XX

PT A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.

XX Disclosure; Page 179-180; 243pp; English.

XX The present invention describes a composition (C) for enhancing an immune
XX response against an antigen or a virus-like particle in an animal. (C)
XX comprises a virus-like particle (VLP) bound to at least one antigen, or a
XX VLP capable of being recognised by the immune system of the animal. Also
XX described: (1) enhancing an immune response against an antigen or a VLP
XX in an animal comprising introducing (C) into the animal; (2) vaccines
XX comprising (C) together with a pharmaceutical diluent, carrier or
XX excipient; (3) immunising or treating an animal comprising administering
XX the vaccine to the animal, or priming or boosting a T cell response in
XX the animal by administering the vaccine; and (4) enhancing anti-viral
XX protection in an animal comprising introducing (C) into the animal. (C)
XX has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
XX antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
XX antihypertensive, antidiabetic, neuroprotective, nootropic, osteoprotic,
XX antirheumatic and antiarthritic activities. (C) or the vaccines can be
XX used for enhancing an immune response against an antigen or a VLP in an
XX animal, enhancing anti-viral protection in an animal, or immunising or
XX treating tumors and infectious diseases such as viral, bacterial,
XX parasitic or fungal infections. The vaccine compositions are also useful
XX for preventing or treating allergies, drug addiction, graft-versus-host
XX disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
XX Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
XX autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

DB 1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKQVKIONPACTANGSCDPSVTROKAYADYTFSTQSTDEBAFVATELAALASPL 120
DB 61 NYKQVKIONPACTANGSCDPSVTROKAYADYTFSTQSTDEBAFVATELAALASPL 120

QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 4
ABU09689
ID ABU09689 standard; protein; 132 AA.
XX

XX ABU09689;
XX

XX 03-JUL-2003 (first entry)
XX

XX Bacteriophage Qbeta mutant coat protein #1.
XX

XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
XX cardiatic; nephrotoxic; ophthalmological; immunostimulant; vaccine;
XX angiotensin peptide moiety carrier conjugate; angiotensin peptide;
XX renin-activated angiotensin system; hypertension; stroke; infarction;
XX congestive heart failure; kidney failure; retinal haemorrhage; mutant;
XX muteln.

XX Bacteriophage Qbeta.
XX

XX WO2003031466-A2.
XX

XX 17-APR-2003.
XX

XX 07-OCT-2002; 2002WO-EP011219.
XX

XX 05-OCT-2001; 2001US-0326998P.
XX

XX 07-NOV-2001; 2001US-0331045P.
XX

XX 18-JAN-2002; 2002US-00050902.
XX

XX 21-JAN-2002; 2002WO-IB000166.
XX

XX 19-JUL-2002; 2002US-0396637P.
XX

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX

XX Bachmann M;
XX

XX WPI; 2003-430264/40.
XX

XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
XX an angiotensin peptide moiety, useful for treating or preventing a
XX disorder associated with renin-activated angiotensin, e.g. hypertension
XX or infarction.

XX Claim 20; Page 93-94; 97pp; English.

XX The invention describes an angiotensin peptide moiety carrier conjugate
XX comprising: (a) a carrier with at least one first attachment site; and
XX (b) at least one angiotensin peptide moiety with at least one second
XX attachment site. The angiotensin peptide moiety and compositions
XX comprising them are useful for immunising an animal against an
XX angiotensin peptide, and for treating or preventing a physical disorder
XX associated with renin-activated angiotensin system such as hypertension,
XX stroke, infarction, congestive heart failure, kidney failure, and retinal
XX haemorrhage. The conjugate is also useful for inducing immune responses,
XX including producing antibodies. This is the amino acid sequence of a
XX mutant bacteriophage Qbeta coat protein used in the preparation of the
XX vaccine conjugates of the invention
XX
XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 AKLEVTTLGNIGDGGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NKKVQVKIONPFACTNNGSCDPSVTROKADVTFSFTQYSTDBERAFVTELAALASPL 120
 DB 61 NKKVQVKIONPFACTNNGSCDPSVTROKADVTFSFTQYSTDBERAFVTELAALASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 5
 ABR44555
 ID ABR44555 standard; protein; 132 AA.
 XX
 AC ABR44555;
 XX
 DT 25-JUL-2003 (first entry)
 XX
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:23.
 XX
 KM Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KM hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KM immunostimulant; cytotoxic; antiallergic; virucide; antibacterial;
 KM immune response; immunisation; allergy; tumour; breast cancer;
 KM neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KM chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 PN MO2003024481-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 16-SEP-2002; 2002MO-IB004132.
 XX
 PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR) MAURER P.
 PA (TISS) TISSOT A.
 PA (SCHW) SCHWARZ K.
 PA (MEID) MEIERINK E.
 PA (LIP) LIPOMSKY G.
 PA (PUMP) PUMPENS P.
 PA (CIEL) CIELENS I.
 PA (RENF) RENHOFA R.
 XX
 PI Maurer P, Tissot A, Schwarz K, Meierink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
 XX
 DR WPI; 2003-354564/33.
 XX
 PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 PS Disclosure; Page 259; 322pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the vaccine;
 CC vaccine. (C) has immunostimulant, cytotoxic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best local similarity 100.0%; Pred. No. 1.1e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 AKLEVTTLGNIGDGGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NKKVQVKIONPFACTNNGSCDPSVTROKADVTFSFTQYSTDBERAFVTELAALASPL 120
 DB 61 NKKVQVKIONPFACTNNGSCDPSVTROKADVTFSFTQYSTDBERAFVTELAALASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 6
 ADD24130
 ID ADD24130 standard; protein; 132 AA.
 XX
 AC ADD24130;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Bacteriophage Qbeta coat protein mutant Qbeta-240.
 XX
 KM vaccine composition; virus-like particle; core particle;
 KM first attachment site; antigen; antigenic determinant; prion protein;
 KM PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KM prion disease; Bovine Spongiform Encephalopathy; BSE;
 KM Creutzfeldt-Jakob Disease; coat protein; mutant; mutcin.
 XX
 OS Synthetic.
 OS Bacteriophage Qbeta.
 XX
 PN MO2003059386-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003MO-EB000460.
 XX
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002MO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR) MAURER P.
 PA (PELL) PELLICOLI E.
 PI Bachmann M, Maurer P, Pellicoli E, Renner WA;
 XX
 DR WPI; 2003-598483/56.
 XX
 PT A vaccine composition for preventing or treating prion diseases (e.g.

PT Creutzfeldt-Jacob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

Example 1; SEQ ID NO 23; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (PrP) or its dimer, or a PrP peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jacob Disease. The present sequence is the amino acid sequence of a mutant coat protein from bacteriophage Obea which may be used during the creation of the vaccine composition of the invention.

XX SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
DB 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
DB 61 NKKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 7
ADJ82056
ID ADJ82056 standard; protein; 132 AA.

XX ADJ82056;
AC
XX
XX
DT 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

XX osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.

XX Unidentified.

OS WO2003039225-A2.

PN 15-MAY-2003.

PD 07-NOV-2002; 2002WO-EP012449.

PF 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-44130/41.

PT New compositions comprising a core particle and at least one antigen or
PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
PT of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 23; 222pp; English.

XX The invention relates to a composition comprising a core particle having
CC at least one first attachment site, and at least one antigen or antigenic
CC determinant having at least one second attachment site. The antigen or
CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
CC peptide. The second attachment site is (non-) naturally occurring with
CC the antigen or antigenic determinant, and is capable of association to
CC the first attachment site. The antigen or antigenic determinant and the
CC core particle interact through the association to form an ordered and
CC repetitive antigen array. The composition is useful as a medicament, or
CC for the manufacture of a medicament for treating bone diseases. The
CC composition is especially useful for as a vaccine for therapy or
CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
CC and for stimulating mammalian immune system. This sequence represents a
CC protein of the invention.

XX SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
DB 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
DB 61 NKKVQVKIONPRACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 8
ADK17144
ID ADK17144 standard; peptide; 132 AA.

XX ADK17144;
AC
XX
XX
DT 06-MAY-2004 (first entry)

DE Virus-like particle repetitive antigen array peptide #23.

XX antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
KW interleukin; IL-5; IL-13; ectatin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

OS WO2003040164-A2.

PN 15-MAY-2003.

PD 07-NOV-2002; 2002WO-EP012455.

PF 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Jennings G, Sonderegger I;

XX WPI; 2003-441518/41.

PT Composition comprising an ordered and repetitive antigen or antigenic
PT determinant array, useful as a medicament, or for manufacturing a
PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's Lymphoma.
XX
PS Disclosure; SEQ ID NO 23; 245pp; English.
XX
CC The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments; or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70; Mismatches 0; Gaps 0;
Matches 132; Conservative 0; Indels 0; Gaps 0;
QY 1 AKLETWTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
1 AKLETWTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBARFVTELAALLASPL 120
61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBARFVTELAALLASPL 120
QY 121 LIDALDQLNPAY 132
121 LIDALDQLNPAY 132
Db 121 LIDALDQLNPAY 132
121 LIDALDQLNPAY 132
RESULT 9
ADJ36313
ID ADJ36313 standard; protein; 132 AA.
XX
AC ADJ36313;
XX
DT 22-APR-2004 (first entry)
XX
DE Bacteriophage AP205 coat protein virus-like particle.
XX
KM antiallergic; cytostatic; virucide; immunostimulant; vaccine;
KM immune response; virus-like particle; immunostimulatory; allergy; tumour;
KM chronic disease; chronic viral disease; RNA bacteriophage; coat protein;
KM VLP; adjuvant.
XX
OS Bacteriophage AP205.
XX
PN WO2004000351-A1.
XX
PD 31-DEC-2003.
XX
PP 20-JUN-2003; 2003WO-EP006541.
XX
PR 20-JUN-2002; 2002US-0389898P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Renner WA;
XX
DR WPI; 2004-108361/11.
XX
PT New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
PS Disclosure; SEQ ID NO 14; 252pp; English.
XX
CC The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of an RNA bacteriophage
CC coat protein a virus like particle (VLP) that can be used in the adjuvant
CC of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70; Mismatches 0; Gaps 0;
Matches 132; Conservative 0; Indels 0; Gaps 0;
QY 1 AKLETWTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
1 AKLETWTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBARFVTELAALLASPL 120
61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBARFVTELAALLASPL 120
QY 121 LIDALDQLNPAY 132
121 LIDALDQLNPAY 132
Db 121 LIDALDQLNPAY 132
121 LIDALDQLNPAY 132
RESULT 10
ADJ67159
ID ADJ67159 standard; protein; 132 AA.
XX
AC ADJ67159;
XX
DT 06-MAY-2004 (first entry)
XX
DE Phage Qbeta coat protein mutant Qbeta 240 for antigen display array.
XX
KM anorectic; core particle; antigenic determinant; ghrelin; P-pillin;
KM antigenic array.
XX
OS Bacteriophage Qbeta.
OS Synthetic.
XX
PN WO2004009124-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-EP007849.
XX
PR 19-JUL-2002; 2002US-0396638P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Fulurija A;
XX
DR WPI; 2004-132866/13.
XX
PT New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.
XX
PS Disclosure; SEQ ID NO 17; 175pp; English.
XX
CC The invention relates to a new composition comprising: (i) a core
CC particle with at least one first attachment site; and (ii) at least one
CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the ghrelin or a
 CC ghrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC Qbeta coat protein mutant which can used as part of the repetitive or
 CC antigenic array.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 1.1e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAQAVPALERKRVTVSVSQPSRRNK 60
 DB 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAQAVPALERKRVTVSVSQPSRRNK 60

QY 61 NKVVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALLASPL 120
 DB 61 NKVVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALLASPL 120

QY 121 LIDAIIDQINPAY 132
 DB 121 LIDAIIDQINPAY 132

RESULT 11
 ADK52193

ID ADK52193 standard; protein; 132 AA.

XX ADK52193;

DT 20-MAY-2004 (first entry)

DE Bacteriophage Qbeta coat protein mutant K13R.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
 KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
 KW coat protein; CP; mutant; mutein.

XX Bacteriophage Qbeta.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 13 /note= "Wild type Lys substituted by Arg"

FT WO2004016282-A1.

PD 26-FEB-2004.

PF 18-JUL-2003; 2003WO-EP007864.

PR 19-JUL-2002; 2002US-0396639P.

PR 15-MAY-2003; 2003US-0470432P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARTIS PHARMA AG.

PI Bachmann MF, Tissot A, Ortman R, Lucend R, Staufenbiel M;
 PI Frey P;

DR MPI; 2004-203731/19.

PT Composition comprising a core particle with at least one attachment site,
 PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 PT such as Alzheimer's disease.

XX Example 1; SEQ ID NO 17; 184pp; English.

XX The invention describes a novel composition comprising a virus-like core
 CC particle with at least one attachment site, and an antigenic amyloid beta
 CC 1-6 peptide. The new composition comprises a core particle with at least
 CC one first attachment site; and at least one antigen or antigenic
 CC determinant with at least one second attachment site, where the antigen
 CC or antigenic determinant is a amyloid beta 1-6 peptide, and where the
 CC second attachment site comprises an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; or an attachment
 CC site naturally occurring with the antigen or antigenic determinant. The
 CC second attachment site is capable of association to the first attachment
 CC site and the beta 1-6 peptide and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC Alzheimer's disease and related diseases. This is the amino acid sequence
 CC of an RNA bacteriophage Qbeta coat protein mutant that can be used in the
 CC preparation of the compositions and vaccines of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 1.1e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAQAVPALERKRVTVSVSQPSRRNK 60
 DB 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAQAVPALERKRVTVSVSQPSRRNK 60

QY 61 NKVVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALLASPL 120
 DB 61 NKVVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALLASPL 120

QY 121 LIDAIIDQINPAY 132
 DB 121 LIDAIIDQINPAY 132

RESULT 12

ID ABG94318 standard; protein; 132 AA.

XX ABG94318;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

DE PDB250 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KW vaccine; infectious disease.

XX unidentified bacteriophage.

PN WO200256905-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002WO-IB000166.

PR 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0288649P.

PR 05-OCT-2001; 2001US-0326998P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Seibel P;
 PI Ploesek C;

DR MPI; 2002-627351/67.

XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 XX
 PS Claim 18; Page 145; 441pp; English.
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)
 XX
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 2,4e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLETTTLGNIGDGKQTLVLRGVPNTGVSLSQAGAVPALERKRVTVSVSQPSRNRK 60
 DB 1 ARLETTTLGNIGDGKQTLVLRGVPNTGVSLSQAGAVPALERKRVTVSVSQPSRNRK 60
 QY 61 NYKVQKIQNPACTANGSCDPSVTROKVDVTFSTQVSTDEBRAPVETELAAALSPL 120
 DB 61 NYKVQKIQNPACTANGSCDPSVTROKVDVTFSTQVSTDEBRAPVETELAAALSPL 120
 QY 121 LIDAIIDQLNPAY 132
 DB 121 LIDAIIDQLNPAY 132
 RESULT 13
 ABG80630
 ID ABG80630 standard; protein; 132 AA.
 XX
 XX ABG80630;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 XX Bacteriophage Q-beta A1 coat protein mutant Qbeta-250.
 DE
 DE Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM immunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 XX
 PN MO200256907-A2.
 XX
 XX
 PD 25-JUL-2002.
 XX
 XX
 PF 21-JAN-2002; 2002WC-IB000168.
 XX
 XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326598P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUBO) LUBOEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 XX
 XX Maurer P, Lechner F, Ortman R, Lucend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Flosek C;
 PI WPI; 2002-636514/68.
 XX
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 XX
 PS Example 18; Page 145; 441pp; English.
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 XX
 XX Sequence 132 AA;
 SQ
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 2,4e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLETTTLGNIGDGKQTLVLRGVPNTGVSLSQAGAVPALERKRVTVSVSQPSRNRK 60
 1 ARLETTTLGNIGDGKQTLVLRGVPNTGVSLSQAGAVPALERKRVTVSVSQPSRNRK 60

DB 1 ARLEVTTLGNIRGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTVSVQSPSRNK 60
 QY 61 NKVKQVKIONPACTANGSCDPSVTRQKADVTFFSTQYSTBERAFVTELAALLASPL 120
 DB 61 NKVKQVKIONPACTANGSCDPSVTRQKADVTFFSTQYSTBERAFVTELAALLASPL 120
 QY 121 LIDAIDQOLNPAY 132
 DB 121 LIDAIDQOLNPAY 132
 RESULT 14
 ABR56454
 ID ABR56454 standard; protein; 132 AA.
 AC ABR56454;
 XX 28-JUL-2003 (first entry)
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO.25.
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KM cytosolic; virucide; antibacterial; antiparasitic; fungicide;
 KM antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
 KM antihydrolytic; antidiabetic; neuroprotective; nootropic; osteopathic;
 KM antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KM inflammatory autoimmune disease.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 OS WO2003024480-A2.
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-IB004252.
 XX 14-SEP-2001; 2001US-0318967P.
 PR (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann MF, Storni T, Lechner F;
 XX MPI; 2003-363095/34.
 DR A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX Disclosure; Page 181; 243pp; English.
 PS The present invention describes a composition (C) for enhancing an immune
 XX response against an antigen or a virus-like particle in an animal. (C)
 XX comprises a virus-like particle (VLP) bound to at least one antigen. (C)
 XX is capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antidiabetic, antinflammatory,
 CC antihydrolytic, antirheumatic, neuroprotective, nootropic, osteopathic,
 CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,

CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 2.4e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLEVTTLGNIRGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTVSVQSPSRNK 60
 DB 1 ARLEVTTLGNIRGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTVSVQSPSRNK 60
 QY 61 NKVKQVKIONPACTANGSCDPSVTRQKADVTFFSTQYSTBERAFVTELAALLASPL 120
 DB 61 NKVKQVKIONPACTANGSCDPSVTRQKADVTFFSTQYSTBERAFVTELAALLASPL 120
 QY 121 LIDAIDQOLNPAY 132
 DB 121 LIDAIDQOLNPAY 132
 RESULT 15
 ABU09691
 ID ABU09691 standard; protein; 132 AA.
 AC ABU09691;
 XX 03-JUL-2003 (first entry)
 DE Bacteriophage Qbeta mutant coat protein #3.
 XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KM cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KM renin-activated angiotensin system; hypertension; stroke; infarction;
 KM congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KM
 XX Bacteriophage Qbeta.
 OS WO2003031466-A2.
 XX 17-APR-2003.
 PD 07-OCT-2002; 2002WO-EP011219.
 XX 05-OCT-2001; 2001US-0326988P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M;
 XX MPI; 2003-430264/40.
 DR New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX Claim 20; Page 94; 97pp; English.
 PS The invention describes an angiotensin peptide moiety carrier conjugate
 CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second

CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage Obeta coat protein used in the preparation of the
CC vaccine conjugates of the invention
XX
SQ Sequence 132 AA;

Query Match 99.5%; Score 661; DB 6; Length 132;
Best Local Similarity 99.2%; Pred. No. 2,4e-70;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	AKLETVTLGNI	GRD	GKQ	TLV	IN	PR	GVN	PT	NG	VAS	LS	Q	AG	AV	P	AL	E	K	R	V	T	V	S	Q	P	S	R	N	R	K	60
DB	1	ARLETVTLGNI	GRD	GKQ	TLV	IN	PR	GVN	PT	NG	VAS	LS	Q	AG	AV	P	AL	E	K	R	V	T	V	S	Q	P	S	R	N	R	K	60
QY	61	NYKVQVKIQN	PT	ACT	ANG	SCD	P	SV	T	R	Q	K	V	A	D	T	F	S	F	T	Q	S	T	D	E	R	A	F	V	T	E	L
DB	61	NYKVQVKIQN	PT	ACT	ANG	SCD	P	SV	T	R	Q	K	V	A	D	T	F	S	F	T	Q	S	T	D	E	R	A	F	V	T	E	L
QY	121	LIDAI	D	O	L	N	P	A	Y																							
DB	121	LIDAI	D	O	L	N	P	A	Y																							

Search completed: January 4, 2005, 09:11:00
Job time : 40.6824 secs


```
FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2
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Query Match 12.3%; Score 81.5; DB 4; Length 626;

Best Local Similarity 22.0%; Pred. No. 0.3; Mismatches 44; Indels 35; Gaps 5;

Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

```
13 RDGKQTLVL-----NPGVPTNGVASLSQAG-----VPALSKRV 48
138 KDNENYIVVEKKKKKINQNNADQVNAISSLYPGALVYANGSEIVENQPDVLPVRRDSL 197
49 TVSVSOPSRNRKRYKQVQKIQNPACTANGSCDPSVTR-----QKADYTFSTQYSTD 102
198 TLEIDLEGMNQDNKIVK--NATKSNVNNAVNTLVYERMEKXYAQAPNVS---AKIDYD 252
QY 103 EERAFVRETELA 114
DB 253 DEMAYSESQULA 264
```

RESULT 3

```
US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249
```

Query Match 11.3%; Score 75; DB 4; Length 409;

Best Local Similarity 25.2%; Pred. No. 1; Mismatches 51; Indels 22; Gaps 5;

Matches 31; Conservative 19; Mismatches 51; Indels 22; Gaps 5;

```
13 RDGKQTLVLNPR-----GVNPTNGVASLSQAGAVPALSKRVTV-SVSOPSRNRKRYKQ 65
118 RCGRLVNVNPRNALLSFANVPVDTGTPV-----IAKPNQRLITRIDLLAPGRGNSN---A 169
QY 66 VKQNPACTANGSCDPSVTRQKADYTFSTQYSTDEERAFVRETELAALLASPLIDAI 125
DB 170 IAVIRETGFNNALVVENTAKPYSEITP-----EEVMSYKTAHMLKASKQIIDL 222
QY 126 DQI 128
DB 223 POL 225
```

```
RESULT 4
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637
```

Query Match 10.8%; Score 71.5; DB 4; Length 916;

Best Local Similarity 22.9%; Pred. No. 10; Mismatches 53; Indels 21; Gaps 4;

Matches 27; Conservative 17; Mismatches 53; Indels 21; Gaps 4;

```
9 GNIGRDG-----KQTLVNPGRVPTNGVASLSQAGAVPALSKRVTVSVS-----OP 55
789 GLTGSGALRLRAALVQARRIDPQGLAALPLVQGLPALLQABDFARGSLDQWQA 848
QY 56 SRNRKRYKQVQKIQNPACTANGSCDPSVTRQKADYTFSTQYSTDEERAFVRETE 110
DB 849 EERGAERYAQSAREHREHPCRSIEANADCPISADAGRW-----PWTFSDSATRWALRT 901
```

RESULT 5

```
US-09-270-767-44620
Sequence 44620, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44620
LENGTH: 502
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44620
```

Query Match 10.6%; Score 70.5; DB 4; Length 502;

Best Local Similarity 24.2%; Pred. No. 5.4; Mismatches 52; Indels 19; Gaps 4;

Matches 29; Conservative 20; Mismatches 52; Indels 19; Gaps 4;

```
18 TLVLANRGVNPPTNGVASLSQAGAVPALSKRVTVSVSQP-----SRNRKRYKQVQKIQN 70
258 TLAVN---TSPSSPTPOPIVEPEQVENSVTYVASPVPVYAKXANDRKQTRSTIKN 314
QY 71 PFACTANGSCDPSVTRQKADYTFSTQ-----YSTDEERAFVRETELAALLASPL 121
DB 315 AKXVYVFCTSSATHTSRCTSSYVSGSLGSPPLGXADKDFVTTAKPLATFTISSPWL 374
```

RESULT 6

```
US-08-090-148-1
Sequence 1, Application US/08090148
Patent No. 5534257
GENERAL INFORMATION:
```

APPLICANT: Maestico, Robert Allan
APPLICANT: Stockley, Peter George
APPLICANT: Talbot, Simon John
TITLE OF INVENTION: Antigen-Presenting Capsid with
TITLE OF INVENTION: Fusion MS2-Coat Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roseman & Collin
STREET: 575 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10022-2585
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44Mb
COMPUTER: IBM PS2-486
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,148
FILING DATE: 08/11/93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101550.3
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/22/92
ATTORNEY/AGENT INFORMATION:
NAME: Nissenbaum, Israel
REGISTRATION NUMBER: 27,582
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-6636
TELEFAX: (212) 940-6404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: NOT RELEVANT
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: VIRUS
FEATURE:
NAME/KEY: Coat protein from MS2-RNA
NAME/KEY: bacteriophage
LOCATION: Location 1 through 129 below
LOCATION: represents entire MS2 coat
LOCATION: protein in the published
LOCATION: sequence.
PUBLICATION INFORMATION:
AUTHORS: Min Jou, W.; Haegeman, G.;
AUTHORS: Yeebaert, M.; Fiers, W.
TITLE: Nucleotide sequence of the
TITLE: gene coding for the
TITLE: bacteriophage MS2 coat protein
JOURNAL: Nature
VOLUME: 237
PAGES: 82-88
DATE: 1972
US-08-090-148-1

Query Match 10.5%; Score 69.5; DB 1; Length 129;
Best Local Similarity 25.0%; Pred. No. 0.85; Mismatches 24; Conservative 16; Mismatches 43; Indels 13; Gaps 2;

27 NPTNGVA-----SLSGAGVPALEKRVTVSVQPSNRKRVKQVRIQNPACTANGSC 80
24 NPNAGVEMTSSNRSGA-----YKVCVSNGSSAQNKRTTKVVPKVAQTGVGVE 76
81 DPEVTROKVAADVTFSTQYSTDERAFVTEIALLL 116
77 LPVAAMRSYINMETLPIFATNSDCELIVAMOGLL 112

RESULT 7
US-09-302-626B-182
Sequence 182, Application US/09302626B
Patent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Maignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 182
LENGTH: 300
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pepa
US-09-302-626B-182

Query Match 10.4%; Score 69; DB 4; Length 300;
Best Local Similarity 23.2%; Pred. No. 3.7; Mismatches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7;

10 NIGRDKQTLVILNPRGVNPTNGVASLSQAGV-----PALERKRV 49
5 NVHRDGRKQMDSEASAVRT-GAASVSABAARGFMAAFSVLALGVAAFSAPASGII 63
50 VSVSOPSRNR-----KATKQVYKIQNPACTANGSCDPSVTRQKXADVTFSTQYSTDR 103
64 ADKSAKPKNOQAVILQTPANGLPQVNIOTPS-----SQGVSVNR-----FKQPDVDR 108
104 E-----RAFVTRTEIALLL-----ASPLIDAIQOLNPA 131
109 KGVILNRSRNTQTQLGWITQGNPHLARGEARVIVQIDSSNPS 152

RESULT 8
US-09-302-626B-185
Sequence 185, Application US/09302626B
Patent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Maignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 185
LENGTH: 622
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pepa
US-09-302-626B-185

Query Match 10.4%; Score 69; DB 4; Length 622;
Best Local Similarity 23.2%; Pred. No. 12; Mismatches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7;

TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 745
LENGTH: 381
TYPE: PRP
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: SITE
LOCATION: 1...381
OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-745

Query Match 10.3%; Score 68.5; DB 4; Length 381;
Best Local Similarity 19.8%; Pred. No. 6.3;

Matches 26; Conservative 27; Mismatches 63; Indels 15; Gaps 3;

QY 3 LETVTIGNIGRQKQTLVINPBGVNPNGVASLSQAGAVPALEKRYTVSVQPSRRKRY 62
DB 6 VKTVIL-NIGRKILQGIKKKKKIGIXSGLFLDLV-----LLGVSKQRTETSAV 56
QY 63 KQVQKQNPACTANGSCDPSVTRQKYADVTFS-----FTQYSTDEERAFVTELAAL 116
DB 57 KNLREKLAACPKNSASLSAKKSHTKTTPGSIKPSKFDATQDKTFQKTSQAP 116

QY 117 ASPLIDAIQ 127
DB 117 AKETIKELER 127

RESULT 13

US-09-045-186-2
Sequence 2, Application US/09045186

Patent No. 6087154

GENERAL INFORMATION:

APPLICANT: Baez, Melvyn

APPLICANT: Cates, Carolyn A.

TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: 111 Corporate Center

CITY: Indianapolis

STATE: Indiana

COUNTRY: United States of America

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/045,186

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: P-11376

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756

TELEFAX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-045-186-2

Query Match 10.3%; Score 68.5; DB 3; Length 383;

Best Local Similarity 25.0%; Pred. No. 6.4;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTVINPBGVNPNTN-----GVA---SLSQAGAVPALEKRYTVSVQPSRRKRYQVK 67

DB 138 RHQLINPBGVNPNNRHAYGVIAVWLVAVASSLPFLIYQ--VMTDEPQN----- 186

QY 68 IONPACTANGSCDPSVTRQKYADVTFSFTQYSTDEERAFVTELAAL 115

DB 187 -----VTIDAYKDKVCFDQPPSDSHRSLYTTLLVL 218

RESULT 14

US-08-232-144-4
Sequence 4, Application US/08232144

Patent No. 5571695

GENERAL INFORMATION:

APPLICANT: SELBIE, Lisa

APPLICANT: HERZOG, Herbert

APPLICANT: SHINE, John

TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figs, Ernst & Kurtz

STREET: 555 13th St, N.W., Suite 701-East

CITY: Washington

STATE: DC

COUNTRY: US

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,144

FILING DATE: 26-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, Barbara G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1871-107A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-232-144-4

Query Match 10.3%; Score 68.5; DB 1; Length 384;
Best Local Similarity 25.0%; Pred. No. 6.4;

Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTVINPBGVNPNTN-----GVA---SLSQAGAVPALEKRYTVSVQPSRRKRYQVK 67

DB 138 RHQLINPBGVNPNNRHAYGVIAVWLVAVASSLPFLIYQ--VMTDEPQN----- 186

QY 68 IONPACTANGSCDPSVTRQKYADVTFSFTQYSTDEERAFVTELAAL 115

DB 187 -----VTIDAYKDKVCFDQPPSDSHRSLYTTLLVL 218

RESULT 15

US-08-555-268A-15

Sequence 15, Application US/08555268A

Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.

APPLICANT: Walker, Mary

APPLICANT: Branchek, Theresa
 APPLICANT: Weinschank, Richard L.
 TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
 TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
 TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/555,268A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 44743-Z/JPM/MAT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0526
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 384 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-555-268A-15

Query Match 10.3%; Score 68.5; DB 2; Length 384;
 Best Local Similarity 25.0%; Pred. No. 6.4;
 Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;
 QY 16 KQTLVNPBGVNPVN-----GVA---SISQAGVPALEKRVTVSVSOPSRRRKRYKVQVK 67
 Db 138 RHQLINRGRPNRRAHYGIAVIWLVAVASSLPFLIYQ--VMTDFPQN----- 186
 QY 68 IQNPTACTANGSCDPSVTROKADVTFSFTQYSTDEERAFVTELAAL 115
 Db 187 -----VTLDAVKDKYVCFDQFSPDSHRLSYTLLVL 218

Search completed: January 4, 2005, 09:35:43
 Job time: 11.3622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-6

Perfect score: 664
Sequence: 1 AKLEVTTLNIGRDKQTLV.....AALASPLLDALDQINPAY 132Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1559051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1559051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	14	US-10-243-739-23
2	664	100.0	132	14	US-10-244-065-23
3	664	100.0	132	14	US-10-289-454-23
4	664	100.0	132	14	US-10-050-902-255
5	664	100.0	132	14	US-10-050-898-255
6	664	100.0	132	14	US-10-346-190-23
7	664	100.0	132	15	US-10-465-811-14
8	664	100.0	132	15	US-10-289-456-23
9	664	100.0	132	15	US-10-622-064-6
10	664	100.0	132	15	US-10-622-124-17
11	664	100.0	132	16	US-10-622-087-17
12	661	99.5	132	14	US-10-243-739-25
13	661	99.5	132	14	US-10-244-065-25

14	661	99.5	132	14	US-10-289-454-25	Sequence 25, App1
15	661	99.5	132	14	US-10-050-902-257	Sequence 257, App
16	661	99.5	132	14	US-10-050-898-257	Sequence 257, App
17	661	99.5	132	14	US-10-346-190-25	Sequence 16, App1
18	661	99.5	132	15	US-10-465-811-16	Sequence 25, App1
19	661	99.5	132	15	US-10-289-456-25	Sequence 8, App1
20	661	99.5	132	15	US-10-622-064-8	Sequence 19, App1
21	661	99.5	132	15	US-10-622-124-19	Sequence 19, App1
22	661	99.5	132	16	US-10-622-087-19	Sequence 26, App1
23	658	99.1	132	14	US-10-243-739-26	Sequence 26, App1
24	658	99.1	132	14	US-10-244-065-26	Sequence 26, App1
25	658	99.1	132	14	US-10-289-456-26	Sequence 26, App1
26	658	99.1	132	14	US-10-050-902-259	Sequence 259, App
27	658	99.1	132	14	US-10-050-898-259	Sequence 259, App
28	658	99.1	132	14	US-10-346-190-26	Sequence 26, App1
29	658	99.1	132	15	US-10-465-811-17	Sequence 17, App1
30	658	99.1	132	15	US-10-289-456-26	Sequence 26, App1
31	658	99.1	132	15	US-10-622-064-9	Sequence 9, App1
32	658	99.1	132	15	US-10-622-124-20	Sequence 20, App1
33	658	99.1	132	16	US-10-622-087-20	Sequence 20, App1
34	655	98.6	132	14	US-10-243-739-10	Sequence 24, App1
35	655	98.6	132	14	US-10-243-739-24	Sequence 24, App1
36	655	98.6	132	14	US-10-243-739-27	Sequence 27, App1
37	655	98.6	132	14	US-10-244-065-10	Sequence 10, App1
38	655	98.6	132	14	US-10-244-065-24	Sequence 24, App1
39	655	98.6	132	14	US-10-244-065-27	Sequence 27, App1
40	655	98.6	132	14	US-10-289-454-10	Sequence 10, App1
41	655	98.6	132	14	US-10-289-454-24	Sequence 24, App1
42	655	98.6	132	14	US-10-289-454-27	Sequence 27, App1
43	655	98.6	132	14	US-10-050-902-159	Sequence 159, App
44	655	98.6	132	14	US-10-050-902-256	Sequence 256, App
45	655	98.6	132	14	US-10-050-902-258	Sequence 258, App

ALIGNMENTS

RESULT 1
US-10-243-739-23
; Sequence 23, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornli, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 23
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2, 1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLNIGRDKQTLVLPNGVNPPTNGVSLGSAQGVLPALERKRVVVSQPSRNK 60
DB 1 AKLEVTTLNIGRDKQTLVLPNGVNPPTNGVSLGSAQGVLPALERKRVVVSQPSRNK 60
QY 61 NKVVQKINPACTNGSCDPSVTRQKADYVFTSFQSTDEERAFVTEALALASPL 120
DB 61 NKVVQKINPACTNGSCDPSVTRQKADYVFTSFQSTDEERAFVTEALALASPL 120
QY 121 LLDALDQINPAY 132

Db 121 LIDAIQDLPAY 132

RESULT 2
US-10-244-065-23

Sequence 23, Application US/10244065
Publication No. US2003009668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Clelens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
DB 1 AKLETVLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
QY 61 NYKVQVQIONPTACTANGSCDPSVTROKXADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQVQIONPTACTANGSCDPSVTROKXADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 3
US-10-289-454-23

Sequence 23, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderesger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
PRIOR FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-240
US-10-289-454-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
DB 1 AKLETVLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
QY 61 NYKVQVQIONPTACTANGSCDPSVTROKXADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQVQIONPTACTANGSCDPSVTROKXADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 4

US-10-050-902-255
Sequence 255, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Sebbel, Peter
APPLICANT: Plosek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 255
LENGTH: 132
TYPE: PRT
ORGANISM: QB 240
US-10-050-902-255

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
DB 1 AKLETVLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSNRK 60
QY 61 NYKVQVQIONPTACTANGSCDPSVTROKXADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQVQIONPTACTANGSCDPSVTROKXADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 5
US-10-050-898-255
; Sequence 255, Application US/10050898
; Publication No. US200301571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisbet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Ploesek, Christine
; APPLICANT: Ottmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.019005
; CURRENT APPLICATION NUMBER: US/10/050, 898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Ob 240
US-10-050-898-255

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGGKQTLVLRGNVPPTNGVASLSQAGVPLERKVTYSVSQPSNRK 60
DB 1 AKLETTTGNIGDGGKQTLVLRGNVPPTNGVASLSQAGVPLERKVTYSVSQPSNRK 60

QY 61 NYKVQKIQNPFTACTANGSCDPSVTROKADVTFSFTQYSTDEBRAFVRELAALASPL 120
DB 61 NYKVQKIQNPFTACTANGSCDPSVTROKADVTFSFTQYSTDEBRAFVRELAALASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 6
US-10-346-190-23
; Sequence 23, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0280003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Ob 240
US-10-346-190-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGGKQTLVLRGNVPPTNGVASLSQAGVPLERKVTYSVSQPSNRK 60
DB 1 AKLETTTGNIGDGGKQTLVLRGNVPPTNGVASLSQAGVPLERKVTYSVSQPSNRK 60

QY 61 NYKVQKIQNPFTACTANGSCDPSVTROKADVTFSFTQYSTDEBRAFVRELAALASPL 120
DB 61 NYKVQKIQNPFTACTANGSCDPSVTROKADVTFSFTQYSTDEBRAFVRELAALASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 7
US-10-465-811-14
; Sequence 14, Application US/10465811
; Publication No. US2004000538A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-465-811-14

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGGKQTLVLRGNVPPTNGVASLSQAGVPLERKVTYSVSQPSNRK 60
DB 1 AKLETTTGNIGDGGKQTLVLRGNVPPTNGVASLSQAGVPLERKVTYSVSQPSNRK 60

QY 61 NYKVQKIQNPFTACTANGSCDPSVTROKADVTFSFTQYSTDEBRAFVRELAALASPL 120
DB 61 NYKVQKIQNPFTACTANGSCDPSVTROKADVTFSFTQYSTDEBRAFVRELAALASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 8
US-10-289-456-23
; Sequence 23, Application US/10289456

Publication No. US2004003211A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 240 mutant
US-10-289-456-23

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
QY 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132

RESULT 9
US-10-622-064-6
Sequence 6, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,575
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-622-064-6

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60

DB 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
1 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132

RESULT 10
US-10-622-124-17
Sequence 17, Application US/10622124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurija, Alma
TITLE OF INVENTION: Ghrelin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,638
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-622-124-17

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
QY 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132

RESULT 11
US-10-622-087-17
Sequence 17, Application US/10622087
Publication No. US20040141964A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tissot, Alain
APPLICANT: Ortman, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Straufenbiel, Matthias
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17

LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-622-087-17

Query Match 100.0%; Score 664; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
DB 1 ARLETVTLNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
QY 121 LIDAIDQNLNPAAY 132
DB 121 LIDAIDQNLNPAAY 132

RESULT 12
US-10-243-739-25
Sequence 25, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243, 739.
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318, 967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-25

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
DB 1 ARLETVTLNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
QY 121 LIDAIDQNLNPAAY 132
DB 121 LIDAIDQNLNPAAY 132

RESULT 13
US-10-244-065-25
Sequence 25, Application US/10244065
Publication No. US20030099668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain

APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Ctelens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244, 065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374, 145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318, 994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-25

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
DB 1 ARLETVTLNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALASPL 120
QY 121 LIDAIDQNLNPAAY 132
DB 121 LIDAIDQNLNPAAY 132

RESULT 14
US-10-289-454-25
Sequence 25, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sondergeger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Boshophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289, 454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396, 636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050, 902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331, 045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-250
US-10-289-454-25

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTTGNIGDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60

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Db      1 ARLETVTLGNIGRGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSTOYSTDERAFVRTLAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSTOYSTDERAFVRTLAALLASPL 120
QY      121 LIDAIQDLNPAY 132
Db      121 LIDAIQDLNPAY 132
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RESULT 15

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US-10-050-902-257
; Sequence 257, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisseot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050.902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-050-902-257
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Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ARLETVTLGNIGRGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSNRK 60
Db      1 ARLETVTLGNIGRGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSTOYSTDERAFVRTLAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSTOYSTDERAFVRTLAALLASPL 120
QY      121 LIDAIQDLNPAY 132
Db      121 LIDAIQDLNPAY 132
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Search completed: January 4, 2005, 09:41:21
Job time : 32.7351 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.86938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-6
Perfect score: 664
Sequence: 1 AKLEVTTLGNIGRDKQTLV.....ALLASPLLIDAIQNLNAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79;+
1: p1r1: +
2: p1r2: +
3: p1r3: +
4: p1r4: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	98.6	132	1	VCBPOB
2	529.5	79.7	131	1	S01964
3	116	17.5	131	1	VCBPR1
4	87.5	13.2	530	2	S22340
5	85.5	12.9	540	2	T00646
6	81.5	12.3	529	2	S24231
7	81.5	12.3	529	2	A43505
8	81.5	12.3	529	2	AC1100
9	81	12.2	830	2	S57537
10	80.5	12.1	1502	1	RGBYH1
11	77.5	11.7	528	2	S22341
12	77	11.6	432	2	T31660
13	76.5	11.5	136	2	C98221
14	76.5	11.5	136	2	AE3065
15	76.5	11.5	1052	2	C64221
16	76	11.4	130	1	A46324
17	76	11.4	282	2	A10186
18	75.5	11.4	1097	2	AD2572
19	75	11.3	130	1	VCBPGA
20	74.5	11.2	130	1	VCBPR
21	74.5	11.2	161	4	T53480
22	74.5	11.2	458	2	T49114
23	74.5	11.2	1861	2	T13845
24	74	11.1	340	2	S18650
25	74	11.1	340	2	A42008
26	74	11.1	366	2	F70618
27	73.5	11.1	520	1	ACMSD1
28	73.5	11.1	601	2	A55921
29	73.5	11.1	654	2	S69673

30	73.5	11.1	719	2	T39271	conserved hypothe
31	73	11.0	243	1	VHUP1	nucleocapsid prote
32	73	11.0	430	2	G88884	protein K09811.10
33	72.5	10.9	129	1	VCBPR2	coat protein - pha
34	72.5	10.9	129	1	VCBPR7	coat protein - pha
35	72.5	10.9	129	1	VCBPR2	coat protein - pha
36	72.5	10.9	289	2	C70400	ferredoxin oxidore
37	72	10.8	248	2	A86786	conserved hypothe
38	72	10.8	1461	2	E90696	hypotheical prote
39	72	10.8	1461	2	A85547	hypotheical prote
40	71.5	10.8	640	2	S48423	hypotheical prote
41	71	10.7	376	2	C84316	hypotheical prote
42	71	10.7	399	1	A43585	polymerase-associa
43	71	10.7	463	2	S00676	translational elonga
44	70.5	10.6	191	2	H90078	hypotheical prote
45	70	10.5	1545	2	T42751	sulfonylurea recep

ALIGNMENTS

RESULT 1
VCBPOB
coat protein - phage Q-beta
C:Species: phage Q-beta
C:Date: 29-Jul-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C:Accession: A92240; A92221; A92088; A04224
R:Escarria, C.; Sasser, P.A.; Billeter, M.A.
J. Biol. Chem. 253, 8390-8399, 1978
A:Title: Determination of the first half of the coat protein cistron of bacteriophage Qb
A:Reference number: A92240; PMID:79048469; PMID:361741
A:Accession: A92240
A:Molecule type: mRNA
A:Residues: 1-80 <ESD>
A:Cross-references: UNIPROT:P03615
R:Stoll, E.; Wilson, K.C.; Reiser, J.; Weissmann, C.
J. Biol. Chem. 252, 990-993, 1977
A:Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.
A:Reference number: A92221; PMID:77118576; PMID:838709
A:Accession: A92221
A:Molecule type: protein
A:Residues: 1-60 <STO>
R:Maite, T.; Konigsberg, W.
J. Biol. Chem. 246, 5003-5024, 1971
A:Title: The amino acid sequence of the Qbeta coat protein.
A:Reference number: A92088; PMID:71288580; PMID:5570434
A:Accession: A92088
A:Molecule type: protein
A:Residues: 1-21, 'D', '23-55, 57-132 <MAI>
C:Superfamily: phage GA coat protein

Query Match 98.6%; Score 655; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 2.6e-57;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	AKLEVTTLGNIGRDKQTLVLRPGVNTGVSLSQAGVPALEKRVTSVQPSNRK	60
DB	1	AKLEVTTLGNIGRDKQTLVLRPGVNTGVSLSQAGVPALEKRVTSVQPSNRK	60
QY	61	NYKQVYKIQNPACTANGSCDPSVTROKADVTFFSTQYSTDERRAFVRELAALLASPL	120
DB	61	NYKQVYKIQNPACTANGSCDPSVTROKADVTFFSTQYSTDERRAFVRELAALLASPL	120
QY	121	LIDAIQNLNAY 132	
DB	121	LIDAIQNLNAY 132	

RESULT 2
S01964
readthrough protein - phage SP
C:Species: phage SP
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

A:Residues: 1-529 <RMS>
A:Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PIDN:CAA42639.1; PID:g44112
A:Experimental source: strain 12057, serotype 4b
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1991
C:Genetics:
A:Gene: lisa
C:Superfamily: dipeptide transport protein
E:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin #status predicted <MAT>

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

Oy 13 RDGQQLVL-----NRGVNPTNGVASLSQAQA-----VPALEKEV 48
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 93 KDGNEIYVEKKKKSINQNADIQVNNAISLTYPGALVKANSELVENPDVLPVRDRL 152
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy 49 TVSVSPSRNRKRYKYQVQVQNPACTANGSCDSBYTR-----OKYADVTSFTQYSND 102
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 153 TLSTLDPGMTGNQDKTVLK--NATKSNVNVNAVNTLVREWNEKTAQAYPNVS--AKIDVD 207
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy 103 EERAFVRTSLAA 114
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 208 DEMAYSESQLIA 219
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
A43505
listeriolysin O precursor - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C:Accession: A43505; S05306; A47606; S12400; A61079
R:Mengaud, J.; Vicensse, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanzy
Infect. Immun. 56, 766-772, 1988
A>Title: Expression in Escherichia coli and sequence analysis of the listeriolysin O de
A:Reference number: A43505; MUID:88153053; PMID:3126142
A:Accession: A43505
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <MEN>
A:Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PIDN:AAA03018.1; PID:g149653
A>Note: This sequence is derived from a strongly hemolytic strain, serotype 1/2c
R:Doman, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A>Title: Nucleotide sequence of the listeriolysin gene from a Listeria monocytogenes ser
A:Reference number: S05306; MUID:89366684; PMID:2505236
A:Accession: S05306
A:Molecule type: DNA
A:Residues: 1-529 <DOM>
A:Cross-references: EMBL:X15127; NID:g44106; PIDN:CAA33223.1; PID:g44107
A:Experimental source: strain EGD
A>Note: This sequence is derived from a weakly hemolytic strain, serotype 1/2a
R:Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cosset, P.
Infect. Immun. 55, 3225-3227, 1987
A>Title: Identification of the structural gene encoding the SH-activated hemolysin of Li
A:Reference number: A47606; MUID:88057627; PMID:2824384
A:Accession: A47606
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 413-480 <ME2>
A:Cross-references: GB:M29171
R:Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cosset, P.
Mol. Microbiol. 4, 2167-2178, 1990
A>Title: Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtain
A:Reference number: S12400; MUID:91211627; PMID:1965218
A:Accession: S12400
A:Molecule type: DNA
A:Residues: 483-493 <MIT>
A:Experimental source: strain LO28, serotype 1/2c
C:Genetics:
A:Gene: hlya; lisa

C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
P:1-25/Domain: signal sequence #status predicted <SIC>
F:26-529/Product: listeriolysin O #status predicted <MAT>

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKOTLVL-----NPRGVNPTNGVASLSQAGA-----VPALEKRY 48
DB 93 KDGNEYIYVEKKKKKINONNMDIQVNAISSLTLYGALVKANSELVENOPDVLPIVRDSL 152
QY 49 TVSVQSPERNKRYVQYKIQNPACTANGSCDPSVTR-----QKYADVTFSFYQSTD 102
DB 153 TLTSIDLPQMTQDNKIVK--NATKSNVNNVAVTLVERNKKYAAQAYPNVS--AKIDYD 207
QY 103 EERAFVTELLA 114
DB 208 DEMAYSESQLIA 219

RESULT 9
S57537
MKTI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N2302; protein YNL085w
C:Species: Saccharomyces cerevisiae
C:Date: 10-Oct-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57537; S50279; S63024; S63017; S65096
R:Solier-Mitz, A.; Sait, J.E.; Ballestra, J.P.G.; Remacha, M.
Submitted to the EMBL Data Library, June 1995
A:Reference number: S57537

C:Superfamily: dipeptide transport protein
A:Gene: hly
C:Superfamily: dipeptide transport protein

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKOTLVL-----NPRGVNPTNGVASLSQAGA-----VPALEKRY 48
DB 93 KDGNEYIYVEKKKKKINONNMDIQVNAISSLTLYGALVKANSELVENOPDVLPIVRDSL 152
QY 49 TVSVQSPERNKRYVQYKIQNPACTANGSCDPSVTR-----QKYADVTFSFYQSTD 102
DB 153 TLTSIDLPQMTQDNKIVK--NATKSNVNNVAVTLVERNKKYAAQAYPNVS--AKIDYD 207
QY 103 EERAFVTELLA 114
DB 208 DEMAYSESQLIA 219

RESULT 8
AC1100
listeriolysin O precursor (imported) - listeria monocytogenes (strain EGD-e)
C:Species: listeria monocytogenes
C:Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1100
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Domingue-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Eutican, K.D.; Fehli, H.; Jones, L.M.; Kars, U.
Science 294, 849-852, 2001
A:Authors: Krell, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Mañeno, E.; Maitournam, A.; Matok, C.; Schuener, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
Article: Comparative genomics of listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <GLA>
A:Cross-references: UNIPROT: P13128; GB: NC_003210; PIDD: CAD00729.1; PID: gl6409567; GSDB: C:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hly

A/Accession: S57537
 A/Molecule type: DNA
 A/Residues: 1-830 <SOL>
 A/Cross-references: UNIPROT:P40850; EMBL:X89016; NID:9887621; PID:9887626
 R/Vermut, M.; Widner, W.R.; Dirmann, J.D.; Wackner, R.B.
 A/Title: Sequence of MKT1, needed for propagation of M(2) satellite dsRNA of the L-A virus
 A/Reference number: S50279; MUID:95176705; PMID:7532890
 A/Accession: S50279
 A/Molecule type: DNA
 A/Residues: 1-29, 'G', 31-808, 'TMTCTCTATYH', <VER>
 A/Cross-references: EMBL:U09129; NID:9520475; PIDN:AA049470.1; PID:9520476
 R/Soler-Mira, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.
 A/Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
 A/Reference number: S65092; MUID:96310628; PMID:8740422
 A/Accession: S65092
 A/Molecule type: DNA
 A/Status: nucleic acid sequence not shown
 A/Residues: 1-830 <SOL>
 A/Cross-references: EMBL:X89016; NID:9887621; PIDN:CAAG1425.1; PID:9887626
 C/Genetics:
 A/Gene: SGD:MKT1
 A/Cross-references: SGD:S0005029; MIPS:YNL085w
 A/Map position: 14L
 C/Superfamily: Saccharomyces cerevisiae MKT1 protein
 C/Keywords: transmembrane protein
 F:615-631/Domain: transmembrane #status predicted <TM>
 Query Match 12.2%; Score 81; DB 2; Length 830;
 Best Local Similarity 25.7%; Pred. No. 7.5;
 Matches 26; Conservative 20; Mismatches 49; Indels 6; Gaps 3;
 Oy 5 TTTTLCNCRDQKQTLVLPKGVNPTNGVSLSQAGVPALEKRTVSVSQPSRRKRYKV 64
 Db 301 STTTON--DSKENQNTQKISALRYKPVLDKTKVLFVQETVSEDESKNNKDK- 356
 Oy 65 QVKIONPACANGSCDPSVTRKAYADVFSTFYOSTDEER 105
 Db 357 KSNLSSPS--SASSASATVTYTKASRKLTKESSTEVK 395
 RESULT 10
 RGBYH1
 C/CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
 N/Alternate names: protein L9672.1; protein YLR256w; regulatory protein CYP1; regulatory
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-SEP-1991 #sequence_revision 23-Feb-1996 #text_change 12-Nov-1999
 C/Accession: S59400; A31312; S15447; S05804; S15446
 R/Johnson, D.
 A/Title: The EMBL Data Library, February 1995
 A/Reference number: S59386
 A/Accession: S59400
 A/Molecule type: DNA
 A/Residues: 1-1502 <JOH>
 A/Cross-references: EMBL:U20865; NID:g662330; PIDN:AAB67387.1; PID:g662331; GSPDB:GN0001

A/Experimental source: strain S288C (AB972)
 R/Pfeifer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
 A/Title: Functional dissection and sequence of yeast HAP1 activator.
 A/Reference number: A31312; MUID:89106221; PMID:2643482
 A/Accession: A31312
 A/Molecule type: DNA
 A/Residues: 1-144, 'T', 146-322, 'R', 324-454, 'N', 456-507, 'W', 509-586, 'K', 588-882, 'N', 884-951
 A/Cross-references: EMBL:U03152; NID:g171645; PIDN:AAA34662.1; PID:g171646
 R/Creusot, R.; Verdier, J.; Gaïgne, M.; Slonimski, P.P.
 J. Mol. Biol. 204, 263-276, 1988
 A/Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
 A/Reference number: S15447; MUID:89125585; PMID:2851658
 A/Accession: S15447
 A/Molecule type: DNA
 A/Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPIME' <CRE1>
 A/Cross-references: EMBL:X13793
 A/Note: the sequence is from mutant CYP1-18
 C/Genetics:
 A/Gene: SGD:HAP1; CYP1; MIPS:YLR256w
 A/Cross-references: SGD:S0004246; MIPS:YLR256w
 A/Map position: 12R
 C/Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology
 C/Keywords: DNA binding; heme binding; transcription regulation; zinc finger
 F:1-148/Domain: DNA binding #status predicted <DNA>
 F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:64-84/Region: zinc finger CCCC motif
 F:177-189/Region: glutamine-rich
 F:245-445/Domain: heme binding #status predicted <HEM>
 F:299-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats
 F:1308-1481/Domain: activation element #status predicted <ACT>
 F:1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
 Best Local Similarity 20.6%; Pred. No. 17;
 Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;
 Oy 23 PRGVN--PTNGVSL-----SQAGVPALEKRTVSVS 53
 Db 1278 PRGISPRKSGSLSSVQPLSSFSMNQNGSTIPVSLNTITSQWGLPDLRTTNQIN 1337
 Oy 54 QPSRNR-KNYKVOYKIQNP-----TACFANGSCDP 82
 Db 1338 LPPSPRDEAFDINSIKQWPTSAFNNANTTIPSTINGNNNNAGTANTDTSANGSALS 1397
 Oy 83 SVTRKAYADY-TSFYOSTD-ERAFVRETLAALASP-LTDAIDQIN 129
 Db 1398 TLTSPOGSDIANSATQYKPDLEDPLMONGNENGLMNPESLVEVGGYN 1447
 RESULT 11
 S22341
 I/vanolysin precursor - Listeria ivanovii
 C/Species: Listeria ivanovii
 C/Date: 07-APR-1994 #sequence_revision 07-APR-1994 #text_change 09-Jul-2004
 C/Accession: S22341; S36683
 A/Reference number: S22340; MUID:92182018; PMID:11543752
 A/Accession: S22341
 A/Molecule type: DNA
 A/Residues: 1-528 <HNS>
 A/Cross-references: UNIPROT:P31831; EMBL:X60461
 A/Note: the authors translated the codon ACA for residue 331 as Val
 R/Kreft, J.
 A/Title: The EMBL Data Library, July 1991
 A/Reference number: S36683
 A/Accession: S36683
 A/Molecule type: DNA
 A/Residues: 1-519, 'T', 321-528 <KRE>
 A/Cross-references: EMBL:X60461
 C/Genetics:

A:Gene: 410
 C:Superfamily: dipeptide transport protein
 F:1-24/Domain: signal sequence <SIG>
 P:25-528/Product: 1vanolysin #status predicted <MKT>

Query Match 11.7%; Score 77.5; DB 2; Length 528;
 Best Local Similarity 21.2%; Pred. No. 9.8;
 Matches 28; Conservative 25; Mismatches 44; Indels 35; Gaps 5;
 QY 13 RGGKQTLV-----NPRGVNPTNGVASLSQAGV-----VPALEKRY 48
 DB 92 KEGNQITVEKKKGSINQNNADIQVINSLSLTPGALVKANSELVENQPDVLPVKRDSY 151
 QY 49 TVSVSQPSRRKRYKQVQKIONFTACTANGSCDPVTR-----QKXADVTFSTQYSTD 102
 DB 152 TISIDLP--GWNHDEIVQVQNTKSNINDGVNLTLDKNNMKYSEEPNIS---AKIDVD 206
 QY 103 EEPAPVETELAA 114
 DB 207 QEMAYSESQVLA 218

RESULT 12

T31660
 hypothetical protein COS41.6 - sea squirt (Cliona intestinalis)
 C:Species: Cliona intestinalis
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T31660
 R:Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Dobson, R.; Tweedie, S.
 Submitted to the EMBL Data Library, December 1996
 A:Reference number: Z21049
 A:Accession: T31660
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-432 <BIR>
 A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CAB0605
 C:Genetics:
 A:introns: 180/2; 212/1; 229/3

Query Match 11.6%; Score 77; DB 2; Length 432;
 Best Local Similarity 27.4%; Pred. No. 8.7;
 Matches 31; Conservative 17; Mismatches 47; Indels 18; Gaps 6;
 QY 4 ETVTLCNIGRDGKQTLVLPNGVNPNGVASLSQAGVPALEKRYTVSVSQPSRRKRYK 63
 DB 242 DTSSEBEVTKDGGNLAENP---TPSNARELOESVASELTETTVKSAIQ--EQDSAYR 297
 QY 64 VQVKIQNPACT--TANGSC-----DPSVTRQRYAD---VTFSTQYSTDE 103
 DB 298 KE-NPQNAACPVRNCGNVCSTNSNKTNPDSKIEIVNDSDDTDEDTQIDTNE 349

RESULT 13

C98221
 hypothetical protein AGR_L_1428 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: C98221
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2333-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; WUID:21608551; PMID:11743194
 A:Accession: C98221
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <NUR>
 A:Cross-references: UNIPROT:Q8UBF3; GB:AE007870; PIDN:AAK8293.1; PID:g15159127; GSPDB:G
 C:Genetics:
 A:Gene: AGR_L_1428
 A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;

Best Local Similarity 24.6%; Pred. No. 2.5;
 Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGRDGKQTLVLPNGVNPNGVASLSQAGV-----PALERKRYTVSVSQPSRRN 59
 DB 3 ISKDGKQTSADPHWLEWVTGTISTLLVAMFGWIAVDIYRSPPEARFEIATVGEGQT 62
 QY 60 KNYKQVQKIQNPACTA-----NGSCDPSTROKADVTFSF--TOYSTDEERAFVTE 111
 DB 63 GQYRVKFAIHNLSMTTAAQVNVKGDLEQNGASPEKNDVTFDYVASSKONGTLFFRSD 120

RESULT 14

AE3065
 conserved hypothetical protein Atcu4139 [imported] - Agrobacterium tumefaciens (strain C5
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AE3065
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCelliff
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; WUID:21608550; PMID:11743193
 A:Accession: AE3065
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <NUR>
 A:Cross-references: UNIPROT:Q8UBF3; GB:AE008689; PIDN:AAL44939.1; PID:g17742593; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atcu4139
 A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;
 Best Local Similarity 24.6%; Pred. No. 2.5;
 Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGRDGKQTLVLPNGVNPNGVASLSQAGV-----PALERKRYTVSVSQPSRRN 59
 DB 3 ISKDGKQTSADPHWLEWVTGTISTLLVAMFGWIAVDIYRSPPEARFEIATVGEGQT 62
 QY 60 KNYKQVQKIQNPACTA-----NGSCDPSTROKADVTFSF--TOYSTDEERAFVTE 111
 DB 63 GQYRVKFAIHNLSMTTAAQVNVKGDLEQNGASPEKNDVTFDYVASSKONGTLFFRSD 120

RESULT 15

C64221
 hypothetical 114K protein (Mgpa 3' region) - Mycoplasma genitalium
 C:Species: Mycoplasma genitalium
 C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C:Accession: C64221; J00092; S18702; S18703
 C:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.A.
 , C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A:Title: The minimal gene complement of Mycoplasma genitalium.
 A:Reference number: A64200; WUID:96026346; PMID:7569993
 A:Accession: C64221
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1052 <TIGR>
 A:Cross-references: UNIPROT:P22747; GB:U39696; GB:L43967; NID:g1045869; PID:g1045877; TIC
 A:Experimental source: strain G-37
 A:Name: J.M.; Loebel, S.; Collier, A.M.; Barile, M.F.; Hu, P.C.
 Gene 82, 259-267, 1989
 A:Title: Nucleotide sequence of the Mgpa (mgp) operon of Mycoplasma genitalium and compa
 A:Reference number: J00090; WUID:9060815; PMID:2583522
 A:Accession: J00092
 A:Molecule type: DNA

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignment)
2094.140 Million cell updates/sec

Title: US-10-622-064-6
Perfect score: 664
Sequence: 1 AALFVTVGNIGRDGKQTLV.....AALLASPLLDALDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_02:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	98.6	132	1	COAT_BPOBE
2	655	98.6	133	2	AAM3126
3	655	98.6	132	2	08LRE1
4	655	98.6	132	2	AAL16663
5	564	84.9	133	2	09TOR9
6	564	84.9	133	2	064307
7	544	81.9	133	2	09TOR9
8	544	81.9	132	1	COAT_BPOBE
9	529.5	79.7	132	1	COAT_BPOBE
10	529.5	79.7	131	1	VAL_BPS
11	496.5	74.8	132	2	09TOR9
12	496.5	74.8	132	2	064310
13	116	17.5	131	1	COAT_BPPRR
14	96.5	14.5	473	1	Q8VDC2
15	87.5	13.2	530	1	TACY_LISSB
16	87.5	13.2	530	2	AAR97361
17	85.5	12.9	540	2	048683
18	82.5	12.4	608	2	084H79
19	82	12.3	325	2	073R79
20	82	12.3	325	2	AAS10709
21	82	12.3	325	2	06HGA7
22	81.5	12.3	529	1	TACY_LISSB
23	81.5	12.3	529	1	TACY_LISSB
24	81.5	12.3	529	2	09L5B9
25	81.5	12.3	529	2	06B9A2
26	81.5	12.3	529	2	06B9A2
27	81.5	12.3	529	2	06B9A2
28	81.5	12.3	529	2	06B9A2
29	81.5	12.3	529	2	06B9A2
30	81.5	12.3	529	2	06B9A2
31	81.5	12.3	529	2	06B9A2

32	81.5	12.3	529	2	06EAB7	06eab7 listeria mo
33	81.5	12.3	529	2	06EAB0	06eab0 listeria mo
34	81.5	12.3	529	2	06EAB4	06eab4 listeria mo
35	81.5	12.3	529	2	06EAB4	06eab4 listeria mo
36	81	12.2	830	1	MKT1_YEAST	P40850 saccharomyc
37	81	12.2	830	2	08TF87	08tf87 saccharomyc
38	81	12.2	830	2	08TF89	08tf89 saccharomyc
39	81	12.2	830	2	08TF89	08tf89 saccharomyc
40	81	12.2	830	2	08TF85	08tf85 saccharomyc
41	81	12.2	830	2	08TF85	08tf85 saccharomyc
42	81	12.2	830	2	AAM00519	Aam00519 drosophila
43	81	12.2	1637	2	09VXK8	09vxk8 drosophila
44	81	12.2	1637	2	09VXK8	09vxk8 drosophila
45	80.5	12.1	1502	1	CYPL_YEAST	P12351 saccharomyc

ALIGNMENTS

RESULT 1
COAT_BPOBE STANDARD; PRT; 132 AA.
ID COAT_BPOBE
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clelens I., Dreilima D., Dislers A., Baumanns V.,
RA One V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmis C., Sastry P.A., Biller M.A.;
RT "Determination of the first half of the coat protein cistron of
RT bacteriophage Q-beta as an application of a mapping procedure for RNA
RT fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll B., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
RT and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiz T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Vallegard K., Liljas L.;
RT "The crystal structure of Bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
- FUNCTION: Forms the phage shell; binds to the phage RNA.

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CC -----

DR EMBL; M99039; AAA1662.1; -.

DR EMBL; V00643; CAA23992.1; -.

DR PIR; A92240; VCBPOB.

DR PDB; 1QBE; X-ray; A/B/C=1-132.

DR InterPro: IPR002703; Levi_coat.

DR Pfam; PF01819; Levi_coat; 1.

KW 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.

FT INIT MET 0 0

FT CONFLICT 22 22 N -> D (in Ref. 4).

FT STRAND 56 56 Missing (in Ref. 4).

FT STRAND 6 9

FT TURN 13 14

FT STRAND 18 27

FT TURN 28 31

FT STRAND 32 36

FT HELIX 42 44

FT STRAND 47 53

FT STRAND 56 56

FT TURN 57 58

FT STRAND 59 59

FT STRAND 62 74

FT STRAND 83 96

FT TURN 98 99

FT HELIX 102 117

FT HELIX 119 126

FT TURN 127 127

SEQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.6%; Score 655; DB 1; Length 132;

Best Local Similarity 98.5%; Pred. No. 8.6e-56;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

DB 1 AKETVTLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

QY 61 NYKQVQKIONPTACTANGSCDPSVTRQKADVTFFSFQYSTDEBERAFVTELAALLASPL 120

DB 61 NYKQVQKIONPTACTANGSCDPSVTRQKADVTFFSFQYSTDEBERAFVTELAALLASPL 120

QY 121 LIDAIQOLNPAY 132

DB 121 LIDAIQOLNPAY 132

RESULT 2

AAAM33126 PRELIMINARY; PRT; 133 AA.

ID AAAM33126

AC AAAM33126; (TREMBlrel. 27, Created)

DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)

DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)

DE Coat protein.

OS Bacteriophage Q-beta.

CC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

CC Alilevirivirus; Alilevirivirus subgroup III.

OX NCBI_TaxID=12009;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=14667253;

RA Bacher J.M., Bull J.J., Ellington A.D.;

RT "Evolution of phage with chemically ambiguous proteomes."

RL BMC Evol. Biol. 3:24-24(2003).

KW Coat protein.

SEQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.6%; Score 655; DB 2; Length 133;

Best Local Similarity 98.5%; Pred. No. 8.7e-56;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

DB 2 AKETVTLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 61

QY 61 NYKQVQKIONPTACTANGSCDPSVTRQKADVTFFSFQYSTDEBERAFVTELAALLASPL 120

DB 62 NYKQVQKIONPTACTANGSCDPSVTRQKADVTFFSFQYSTDEBERAFVTELAALLASPL 121

QY 121 LIDAIQOLNPAY 132

DB 122 LIDAIQOLNPAY 133

RESULT 3

Q8LTEL PRELIMINARY; PRT; 329 AA.

ID Q8LTEL

AC Q8LTEL; (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)

DE A1 read-through protein (A1 protein).

OS Bacteriophage Q-beta.

CC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

CC Alilevirivirus.

OX NCBI_TaxID=12009;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=14667253;

RA Bacher J.M., Bull J.J., Ellington A.D.;

RT "Evolution of phage with chemically ambiguous proteomes."

RL BMC Evol. Biol. 3:24-24(2003).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=4109687; PubMed=7506687;

RA Kozlovskaya T.M., Clemons I., Drellina D., Dieters A., Baumanis V., Ose V., Pumpens P.;

RT "Recombinant RNA phage Q beta capsid particles synthesized and self-assembled in Escherichia coli."

RL Gene 137:133-137(1993).

DR EMBL; AY099114; AAAM33127.1; -.

DR EMBL; M99039; AAA1663.1; -.

DR HSP; P03615; IQBE.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR002703; Levi_coat.

DR InterPro: IPR000504; RNA_Tec_mot.

DR Pfam; PF01819; Levi_coat; 1.

DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

SEQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.6%; Score 655; DB 2; Length 329;

Best Local Similarity 98.5%; Pred. No. 2.5e-55;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

DB 2 AKETVTLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 61

QY 61 NYKQVQKIONPTACTANGSCDPSVTRQKADVTFFSFQYSTDEBERAFVTELAALLASPL 120

DB 62 NYKQVQKIONPTACTANGSCDPSVTRQKADVTFFSFQYSTDEBERAFVTELAALLASPL 121

QY 121 LIDAIQOLNPAY 132

DB 122 LIDAIQOLNPAY 133

RESULT 4

AAAI6663 PRELIMINARY; PRT; 329 AA.

ID AAI6663

AC AAI6663; (TREMBlrel. 27, Created)

DT 02-MAR-2004 (TREMBlrel. 27, Created)

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DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirinae.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9410687; PubMed=7506687;
RA Kozlovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; M99039; AAA16663.1; -.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match          98.6%; Score 655; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 2.5e-55;
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALASPL 120
DB 62 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALASPL 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
ID Q9TOR9;
AC Q9TOR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirinae.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14699.1; -.
DR HSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR InterPro; IPR000504; RNA_rec_mot.
DR POSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match          84.9%; Score 564; DB 2; Length 329;
Best Local Similarity 82.6%; Pred. No. 1.8e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALASPL 120
DB 62 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALADPM 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133

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Query Match          84.9%; Score 564; DB 2; Length 133;
Best Local Similarity 82.6%; Pred. No. 6.3e-47;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALASPL 120
DB 62 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALADPM 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirinae.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14700.1; -.
DR HSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR POSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match          84.9%; Score 564; DB 2; Length 329;
Best Local Similarity 82.6%; Pred. No. 1.8e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALASPL 120
DB 62 NYKVQVQIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTELAAALADPM 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133

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ID	PRELIMINARY;	PRT;	133 AA.
AC	Q970S0		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, last annotation update)		
DE	Coat protein.		
OS	Bacteriophage M11.		
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;		
CC	Allolevivirus.		
OX	NCBI_TaxID=74336;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95239761; PubMed=7723040;		
RA	Beekwilder M.J., Nieuwenhuizen R., van Duin J.;		
RT	"Secondary structure model for the last two domains of single-stranded		
RL	RNA phage Q beta.";		
RN	J. Mol. Biol. 247:903-917(1995).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96190948; PubMed=8609616;		
RA	Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;		
RT	"Secondary structure model for the first three domains of Q beta RNA.		
RL	Control of A-protein synthesis.";		
RN	J. Mol. Biol. 256:8-19(1996).		
RP	[3]		
RP	SEQUENCE FROM N.A.		
RA	Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF052431; AAC06250.1; ..		
DR	HSSP; P03615; IQSE.		
DR	GO; GO:0019028; C:viral capsid; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR02703; Lev1 coat.		
DR	Pfam; PF01819; Lev1_coat; 1.		
KW	Coat protein		
SC	SEQUENCE 133 AA; 14198 MW; 098722E3C6C3A255 CRC64;		
QY	Query Match	81.9%; Score 544; DB 2; Length 133;	
	Best Local Similarity	79.5%; Pred. No. 5, 6e-45;	
	Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;		
DB	1 ALEVTVLGNIGRDRKQTLVLPNGVPTNGVAVSLQGAVALERKRVTVSVSOPSRNRK 60		
	2 AALQAITTSIGICKKGGVTLIDLPNGVPTNGVAAVLSGAVALERKRVTVSVSOPSRNRK 61		
QY	61 NYKVQVAKIQNPACTANGSCDPSVTRKAYADYTFSPQYSTDEERAFVETELAAIIASPL 120		
DB	62 NYKVQVAKIQNPISCTASGTCDSVTRSAVSVDYTFSPQYSTVEERALVTEHALLADPM 121		
QY	121 LIDAIQNLNPAY 132		
DB	122 LVNAIDNLNPAY 133		
RESULT 8			
064303	PRELIMINARY;	PRT;	329 AA.
AC	064303;		
DT	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-AUG-1998 (TREMBLrel. 07, last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)		
DE	Al-protein.		
OS	Bacteriophage M11.		
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;		
CC	Allolevivirus.		
OX	NCBI_TaxID=74336;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95239761; PubMed=7723040;		

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;  

RT "Secondary structure model for the last two domains of single-stranded  

RL RNA phage Q beta.";  

RL J. Mol. Biol. 247:903-917(1995).  

RN [2]  

RP SEQUENCE FROM N.A.  

RX MEDLINE=9619048; PubMed=8609616;  

RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;  

RT "Secondary structure model for the first three domains of Q beta RNA.  

RL J. Mol. Biol. 256:8-19(1996).  

RN [3]  

RP SEQUENCE FROM N.A.  

RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;  

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  

DR EMBL; AF052431; AAC06251.1; -.  

DR HSPB; P03615; IQBE.  

DR GO; GO:0019028; C:viral capsid; IEA.  

DR GO; GO:0005198; F:structural molecule activity; IEA.  

DR InterPro; IPR002703; Levi_coat.  

DR InterPro; IPR005054; RNA_Tec_mot.  

DR Pfam; PF01819; Levi_coat; 1.  

DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.  

SQ SEQUENCE 329..AA; 35893 MW; 3E33CD821EE625F4 CRC64;  

Query Match 81.9%; Score 544; DB 2; Length 329;  

Best Local Similarity 79.5%; Pred. No 1,6e-44;  

Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;  

QY 1 AKLETTVLGNIIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALIEKRVTVSVSQPSHNK 60  

DB 2 AKQAILTSLGKGGKGDVTLDLNPRGVNPTNGVALSBAGAVPALIEKRVTVSVSQPSHNK 61  

QY 61 NYKVQVQKIQNFCTANGSCDPSYTRKQKADVTYPSFYQSTDEBERAFVRIELAAALLASPL 120  

DB 62 NYKVQVQKIQNFCTANGSCDPSYTRSAVSVDYTFSTQYSTVERALVRIELQDLADPM 121  

QY 121 LIDAIQDLNPAV 132  

DB 122 LVNAIDNLNPAV 133  

-----  

RESULT 9  

COAT_BPSP STANDARD; PRT: 132 AA.  

ID_COAT_BPSP  

AC P09673;  

DT 01-MAR-1989 (Rel. 10, Created)  

DT 01-MAR-1989 (Rel. 10, Last sequence update)  

DT 01-FEB-1994 (Rel. 28, Last annotation update)  

DE Coat protein.  

OS Bacteriophage SP.  

DE Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  

OC A11olevivirus.  

OX NCBI_TaxID=12027;  

RN [1]  

RP SEQUENCE FROM N.A.  

RX MEDLINE=86289362; PubMed=339390;  

RA Hirshima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;  

RT "Analysis of the complete nucleotide sequence of the group IV RNA  

RL coliphage SP.";  

RL Nucleic Acids Res. 16:6205-6221(1988).  

RN [1- FUNCTION: Forms the phage shell; binds to the phage RNA.  

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DR EMBL; X07489; CAA30374.1; -.  

DR HSPB; P03615; IQBE.

```

DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
KW Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14129 MW; 50B1B6CC6AF0A254 CRC64;

Query Match 79.7%; Score 529.5; DB 1; Length 132;
Best Local Similarity 78.0%; Pred. No. 1.4e-43;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLSGAGVPALEKRVTVSVQPSNRK 60
DB 2 AKLNQVTLSTIGKNGKGDQTLTLTPRGVNPNGVSLSGAGVPALEKRVTVSVQPSNRK 61
QY 61 NYKVQVIONPTACTANGSCDPSVTRKQVADVTFSTQYSTDERAFVTELALPL 120
DB 62 NFKVQVILQNPACTRD-ACDPSVTRSAFADVTLSTFTSYSTDERALIRTELALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDAILDLNPAY 132

RESULT 10
VAL_BPSP STANDARD; PRT; 331 AA.
AC P09677;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Readthrough protein A1 [Contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC NCBI_TaxID=12027;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hiraehima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).

CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
CC protein sequence.

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CC -----
DR EMBL: X07489; CAB37299.1; -.
DR PIR: S01964; S01964.
DR HSSP: P03615; IOBE.
DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
KW Coat protein.
FT CHAIN 1 132 Coat protein.
FT CHAIN 1 331 Readthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A642E4B52C6582 CRC64;

Query Match 79.7%; Score 529.5; DB 1; Length 331;
Best Local Similarity 78.0%; Pred. No. 4.2e-43;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLSGAGVPALEKRVTVSVQPSNRK 60
DB 2 AKLNQVTLSTIGKNGKGDQTLTLTPRGVNPNGVSLSGAGVPALEKRVTVSVQPSNRK 61
QY 61 NYKVQVIONPTACTANGSCDPSVTRKQVADVTFSTQYSTDERAFVTELALPL 120
DB 62 NFKVQVILQNPACTRD-ACDPSVTRSAFADVTLSTFTSYSTDERALIRTELALADPL 120

DB 62 NFKVQVILQNPACTRD-ACDPSVTRSAFADVTLSTFTSYSTDERALIRTELALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDAILDLNPAY 132

RESULT 11
Q9TOR8 PRELIMINARY; PRT; 132 AA.
ID Q9TOR8
AC Q9TOR8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC NCBI_TaxID=75725;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]

RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059243; AAC14703.1; -.
DR HSSP: P03615; IOBE.

DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
KW Coat protein.

SQ SEQUENCE 132 AA; 14143 MW; 672709375F5F22EA CRC64;

Query Match 74.8%; Score 496.5; DB 2; Length 132;
Best Local Similarity 75.0%; Pred. No. 2.3e-40;
Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLSGAGVPALEKRVTVSVQPSNRK 60
DB 2 AKLNQVTLSTIGKNGKGDQTLTLTPRGVNPNGVSLSGAGVPALEKRVTVSVQPSNRK 61
QY 61 NYKVQVIONPTACTANGSCDPSVTRKQVADVTFSTQYSTDERAFVTELALPL 120
DB 62 NFKVQVILQNPACTRD-ACDPSVTRSGRDVTLSTFTSYSTDERALIRTELALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDAILDLNPAY 132

RESULT 12
O64310 PRELIMINARY; PRT; 330 AA.
ID O64310
AC O64310;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC AlloLevivirus.
 OX NCBI_TaxID=75725;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta."
 RL J. Mol. Biol. 247:903-917(1995).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RL J. Mol. Biol. 256:8-19(1996).
 RN
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF059243; AAC14704.1; -.
 DR HSSP: P03615; 10BE.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR002703; Lev1 coat.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF01819; Lev1_coat_1; UNKNOWN.1.
 DR PROSITE: PS00030; RNM_RNP_1; UNKNOWN.1.
 SQ SEQUENCE 330 AA; 36175 MW; 961E55F40834410 CRC64;
 Query Match 74.8%; Score 496.5; DB 2; Length 330;
 Best Local Similarity 75.0%; Pred. No. 6.8e-40;
 Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKLETVTIGNIGRDGKQTLV--LNPRGVNPTNG--VASISQAGVPALEKRYTVSVSQPSNRK 60
 DB 2 AKLNKVTLTGIGKAGNQTLTLTPRGVNPTNGVASISEAGVPALEKRYTVSVSQPSNRK 61
 QY 61 NYKQVQKQNTACTANGSCDPSVTRKCAVTVTSFTQYSDERAFVTELAALLASPL 120
 DB 62 NYKQVQKQNTACTANGSCDPSVTRKCAVTVTSFTQYSDERAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADININPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR STANDARD; PRT; 131 AA.
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC 1- FUNCTION: Forms the phage shell, binds to the phage RNA.
 DR PIR: A04225; VCBP1.
 DR InterPro: IPR002703; Lev1_coat.
 DR Pfam: PF01819; Lev1_coat_1.
 KW Coat protein; Direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B639E1E50FC612 CRC64;
 OC

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0025;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTVLNRGVNPT-----NGVASISQAGVPALEKRYTVSVSQPSNRKRYVGV 66
 DB 4 QNVLDKREKTPDHFVFPDIDNNGEVESGVPGESRFTLSLKTSGR--YKSTL 61
 QY 67 KIONPT--ACTANGSCDPSVTRKCAVTVTSFTQYSDER--AFVTELAALLASPL 122
 DB 62 KLVVPVQSQTVNGIYTVPVVTRTSYTVDPDYARSTTKERNPFVGMADALADMLVH 121
 QY 123 DAIDQINPAY 132
 DB 122 DTIVNLQGVY 131
 RESULT 14
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (TRENBERE1. 20, Created)
 DT 01-MAR-2002 (TRENBERE1. 20, Last sequence update)
 DT 01-OCT-2003 (TRENBERE1. 25, Last annotation update)
 DE Transmembrane protein 7.
 OS Name="Tmem7";
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 RP SEQUENCE FROM N.A.
 RA STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kies H., Darai E., Kies C., Kost-Alimova M., Klein G., Dumaniski J.P.,
 RA Imreh S.;
 RT "Comparative human/murine sequence analysis of the common eliminated
 RT region 1 from human 3p21.3."
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL: AJ428064; CAD20986.1; -.
 DR MGD: MGI:2446841; Tmem7.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0B69F2A4D CRC64;
 Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.9; Indels 69; Gaps 7;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;
 QY 5 TVTIGNIGRDGKQTLV-----LNPRGVNPTNG--VASISQAGVPALEKRYTVSVSQPSNRK 46
 DB 195 TATCSNLSISSQSPSSKQVQMPQASKANPQASNTKNDPKVSCSKPAPPLSPSLKARAP 254
 QY 47 RYTVSVSQPSNRKRYVGV-----KIONPT--ACTANGSCDPSVTRKCAVTVTSFTQYSDER 87
 DB 255 KYTVTCSNLSISSQSPSSKQVQMPQASKANPQASNTKNDPKVSCSKPAPPLSPSLKARAP 314
 QY 88 -----KYADVTFSTQYSDERAFVTELAALLASPL 122
 DB 315 SPAPAPCTVQMPSPPTIDSGRADYAKENTKSKTRK-----ALLSSPLYV 361
 RESULT 15
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligerialysin precursor (Thiol-activated cytolysin).
 GN Name=L80;
 OS Listeria seeligieri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

Seq	Sequence	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB 261	Length</
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Search completed: January 4, 2005, 09:16:15
Job time : 37.2676 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 ; Search time 98.9054 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKETVTLGNIGKDGKQTL.....FTKPKTKPCPIQAVIVVERA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_GeneSeq_23Sep04.*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	100.0	329	5	ABG94278 Bacterioph
2	1749	100.0	329	5	ABG80590 Bacterioph
3	1749	100.0	329	5	ABU09687 Bacterioph
4	1749	100.0	329	7	ADD24118 Bacterioph
5	1749	100.0	329	7	ADJ82044 Protein f
6	1749	100.0	329	7	ADK17132 Virus-11k
7	1749	100.0	329	8	ADJ36301 Bacterioph
8	1749	100.0	329	8	ADJ67147 Bacterioph
9	1749	100.0	329	8	ADK52181 Bacterioph
10	1733.5	99.1	328	6	ABR56440 Bacterioph
11	1733.5	99.1	328	6	ABR44543 Bacterioph
12	978	55.9	329	6	ABR56445 Bacterioph
13	978	55.9	329	6	ABR44548 Bacterioph
14	978	55.9	329	7	ADD24123 Bacterioph
15	978	55.9	329	7	ADJ82049 Protein f
16	978	55.9	329	7	ADK17137 Virus-11k
17	978	55.9	329	8	ADJ36306 Bacterioph
18	978	55.9	329	8	ADJ67152 Bacterioph
19	978	55.9	329	8	ADK52186 Bacterioph
20	978	55.9	330	5	ABG94315 RNA phage
21	976.5	51.3	331	5	ABG80627 Bacterioph
22	897.5	51.3	330	5	ABG94241 Bacterioph
23	897.5	51.3	330	5	ABG80553 Bacterioph
24	897.5	51.3	330	6	ABR56449 Bacterioph
25	897.5	51.3	330	6	ABR44552 Bacterioph

26	897.5	51.3	330	7	ADD24127 Bacterioph
27	897.5	51.3	330	7	ADJ82053 Protein f
28	897.5	51.3	330	7	ADK17141 Virus-11k
29	897.5	51.3	330	8	ADJ36310 Enterobac
30	897.5	51.3	330	8	ADJ67156 Bacterioph
31	897.5	51.3	330	8	ADK52190 Enterobac
32	663	37.9	132	5	ABG94233 Bacterioph
33	663	37.9	132	5	ABG80545 Bacterioph
34	663	37.9	132	6	ABR56439 Bacterioph
35	663	37.9	132	6	ABU09686 Bacterioph
36	663	37.9	132	6	ABR44542 Bacterioph
37	663	37.9	132	7	ADD24117 Bacterioph
38	663	37.9	132	7	ADD82043 Protein f
39	663	37.9	132	7	ADK17131 Virus-11k
40	663	37.9	132	8	ADJ36300 Bacterioph
41	663	37.9	132	8	ADJ67146 Bacterioph
42	663	37.9	132	8	ADK52180 Bacterioph
43	655	37.4	132	5	ABG94316 POB240 pr
44	655	37.4	132	5	ABG94320 POB251 pr
45	655	37.4	132	5	ABG80632 Bacterioph

ALIGNMENTS

RESULT 1	ABG94278	standard, protein, 329 AA.
ID	ABG94278	
XX	ABG94278	
AC	ABG94278	
DT	06-AUG-2003 (revised)	
DT	10-DEC-2002 (first entry)	
XX		
DE	Bacteriophage Q beta coat protein A1.	
XX		
KW	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory; cytosolic; antiviral; antidiabetic; hypoglycaemic; antigen array; vaccine; infectious disease.	
KW		
OS	Bacteriophage.	
XX		
PN	WO200256905-A2.	
PD		
XX	25-JUL-2002.	
XX		
PF	21-JAN-2002; 2002MO-IB000166.	
XX		
PR	19-JAN-2001; 2001US-0262379P.	
PR	04-MAY-2001; 2001US-0286549P.	
PR	05-OCT-2001; 2001US-0326998P.	
PR	07-NOV-2001; 2001US-0331045P.	
XX		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
XX		
PI	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P; Ploesek C;	
PI	WPI; 2002-627351/67.	
DR		
XX		
PT	Molecular antigen array used in the production of vaccines for infectious diseases.	
XX		
PS	Claim 7; Page 416-417; 44pp; English.	
XX		
CC	This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold comprising a core particle selected from a core particle of a non-natural origin and a core particle of natural origin and an organism comprising at least one first attachment site, where the organism is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment	

site, where the antigen or antigenic determinant is amyloid beta peptide (Abeta1-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Obeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention. (Updated on 06 CC-AUG-2003 to correct OS field.)

SQ Sequence 329 AA;

Query Match	100.0%	Score 1749	DB 5	Length 329
Best Local Similarity	100.0%	Pred. No. 3e-171		
Matches 329	0	Mismatches 0	Indels 0	Gaps 0

QY	MAKLEFVTLTGNGIKGOKGKLTUYNPREBVTNTNGVSLISQAGAVALEKRTVVSQCSRRN	60
Db	1 MAKLEFVTLTGNGIKGOKGKLTUYNPREBVTNTNGVSLISQAGAVALEKRTVVSQCSRRN	60
QY	61 KNYKQVQKIQNFPACTANGSCDBSVTRQAYADVTSEFTQSYDDEEAPFARTEIAALLASP	120
Db	61 KNYKQVQKIQNFPACTANGSCDBSVTRQAYADVTSEFTQSYDDEEAPFARTEIAALLASP	120
QY	121 ILIDAIIDQLNPWYMTLLIAGGGSGSKRPDVPIDPPIIDPPGTGKYTCFPAIWSLEEVEYB	180
Db	121 ILIDAIIDQLNPWYMTLLIAGGGSGSKRPDVPIDPPIIDPPGTGKYTCFPAIWSLEEVEYB	180
QY	181 PPKRMRPPIYNAAVELOPREFDVALKOLLGNTKRRMDSLSYTFPGRCRNGVIIDIDATY	240
Db	181 PPKRMRPPIYNAAVELOPREFDVALKOLLGNTKRRMDSLSYTFPGRCRNGVIIDIDATY	240
QY	241 IATDQAMRDQKDIREGKKPAGFAGNIERFIYILKSINAYCSLSDIAAYHADGVIWGFWRDP	300
Db	241 IATDQAMRDQKDIREGKKPAGFAGNIERFIYILKSINAYCSLSDIAAYHADGVIWGFWRDP	300
QY	301 SSGGALPFPDTKPKDKTKCPIQAIYIVPRA	329
Db	301 SSGGALPFPDTKPKDKTKCPIQAIYIVPRA	329

RESULT 2
ABG80590
ID ABG80590 standard; protein; 329 AA

AC ABG80590;

DT	29-AUG-2003	(revised)
DT	29-NOV-2002	(first entry)

DE Bacteriophage Q-beta A1 protein.

KW Molecular antigen array; vaccine; antigen; antimicrobial;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease; lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy
KW rheumatoid arthritis; diabetes; infectious diseases; factor Xa;
KW enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.

XX
PN W0200256907-A2.

PD 25-JUL-2002

PF 21-JAN-2002; 2002WO-IB000168.

PR 19-JAN-2001; 2001US-0262379P.
DA 04-MAY-2001; 2001ITS-0288549P

PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.

XX (CVT0-) CVTOS BIOTECHNOLOGY PA

PA (NOVS) NOVARTIS PHARMA AG.
PA (MATP/) MATPBB P.

PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN B.

PA (LUEO/) LUEOEND R.
PA (STAIL/) STAUFENBITEL, M.

PA (FREY/) FREY P.
XY

PI Maurer P, Lechner K, Urtzma
PI Penner WA, Bachmann M, Tisse

XX DB WPT: 2002-636514/68.

XX Molecular antigen array used
PT

PT diseases.
XX

PS Disclosure; Page 393-394; 410
XX

CC The invention relates to a com
CC molecular scaffold comprising

core particle or a non-natural origin; and (ii) an organism

CC file, where the organism is
CC one covalent bond; (b) an anti

CC amyloid beta peptide (Abeta)

CC occurring with the antigen on

attachment site naturally occurring with site is capable of association determinant, where the second attachment site is the first attachment site, and through at least one non-peptide bond to the scaffold interact where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. Also included is a process for producing a non-naturally occurring ordered and repetitive antigen array. The composition is used in immunisation and as a vaccine for diseases such as influenza, graft versus host disease, TGF- β -mediated allergic reactions, anaphylaxis, adult respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Graves' disease, systemic lupus erythematosus, inflammatory immune diseases, myasthenia gravis, immunoproliferative disease lymphadenopathy, immunoblastic lymphadenopathy, angioimmunoproliferative lymphadenopathy, scleroderma, Alzheimer's disease, rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis and infectious diseases. The antigens are modified to possess a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N- or C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein). The present sequence is bacterial protein or peptide which is coupled to the modified antigen to form the molecular antigen array. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 329 AA:

Query Match	100.0%	Score 1749	DB 5	length 329
Best Local Similarity	100.0%	Pred. No. 3e-171		
Matches 329; Conservative	0	Mismatches 0	Indels 0	Gaps 0

```
Qy      1 MAKLETVTLLIGNIGKDGGKPTLVLRGRVNPNTGVSLSQAAGVPALAEKRVTIVSVSQPSRRR    60
          |||||
Db      1 MAKLETVTLLIGNIGKDGGKPTLVLRGRVNPNTGVSLSQAAGVPALAEKRVTIVSVSQPSRRR    60
```

```

QY 61 KNYKVQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDEBRAPVRELAALLASP 120
DB 61 KNYKVQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDEBRAPVRELAALLASP 120
QY 121 LLIDAIDQLNPAYWTLTLAGGGSGSKPDVPIPDPIPPPGTGKTCPPAIVMSLEVEVP 180
DB 121 LLIDAIDQLNPAYWTLTLAGGGSGSKPDVPIPDPIPPPGTGKTCPPAIVMSLEVEVP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDATY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDATY 240
QY 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
DB 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTKFDKTCPCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTKFDKTCPCPIQAVIVPRA 329

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RESULT 3

ABU09687
ID ABU09687 standard; protein; 329 AA.

AC ABU09687;

DT 03-JUL-2003 (first entry)

XX Bacteriophage Qbeta coat protein A1.

XX Bacteriophage Qbeta; coat protein; A1; hypotensive; cerebroprotective;
 KW cardiant; nephrotoxic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage.

OS Bacteriophage Qbeta.

XX WO2003031466-A2.

PD 17-APR-2003.

PF 07-OCT-2002; 2002WO-EP011219.

XX 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396637P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M;

XX WPI; 2003-430264/40.

PT New angiotensin peptide moiety carrier conjugate comprising a carrier and
 an angiotensin peptide moiety, useful for treating or preventing a
 disorder associated with renin-activated angiotensin, e.g. hypertension
 or infarction.

XX Claim 16; Page 92-93; 97pp; English.

XX The invention describes an angiotensin peptide moiety carrier conjugate
 comprising: (a) a carrier with at least one first attachment site; and
 (b) at least one angiotensin peptide moiety with at least one second
 attachment site. The angiotensin peptide conjugate and compositions
 comprising them are useful for immunising an animal against an
 angiotensin peptide, and for treating or preventing a physical disorder
 associated with renin-activated angiotensin system such as hypertension,
 stroke, infarction, congestive heart failure, kidney failure, and retinal

CC haemorrhage. The conjugate is also useful for inducing immune response,
 CC including producing antibodies. This is the amino acid sequence of
 CC bacteriophage Qbeta coat protein A1 used in the preparation of the
 CC vaccine conjugates of the invention

XX Sequence 329 AA;

Query Match 100.0%; Score 1749; DB 6; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3e-171;
 Matches 329; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAKETVTLGNIGKQKOTIVNPRGNVPTNGVASTSGAGVPALEKRVTVSVSQPSNR 60
DB 1 MAKETVTLGNIGKQKOTIVNPRGNVPTNGVASTSGAGVPALEKRVTVSVSQPSNR 60
QY 61 KNYKVQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDEBRAPVRELAALLASP 120
DB 61 KNYKVQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDEBRAPVRELAALLASP 120
QY 121 LLIDAIDQLNPAYWTLTLAGGGSGSKPDVPIPDPIPPPGTGKTCPPAIVMSLEVEVP 180
DB 121 LLIDAIDQLNPAYWTLTLAGGGSGSKPDVPIPDPIPPPGTGKTCPPAIVMSLEVEVP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDATY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDATY 240
QY 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
DB 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTKFDKTCPCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTKFDKTCPCPIQAVIVPRA 329

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RESULT 4

ADD24118
ID ADD24118 standard; protein; 329 AA.

XX ADD24118;

DT 15-JAN-2004 (first entry)

DE Bacteriophage Qbeta coat protein A2.

XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; SSE;
 KW Creutzfeldt-Jakob Disease; coat protein.

XX Bacteriophage Qbeta.

OS Bacteriophage Qbeta.

XX WO2003059386-A2.

XX 24-JUL-2003.

PD 17-JAN-2003; 2003WO-EP000460.

XX 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 08-JUL-2002; 2002US-0393725P.

PR 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;

XX WPI; 2003-598483/56.

PT A vaccine composition for preventing or treating prion diseases (e.g.
 Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-

PT phage) and at least one prion protein or peptide bound to the virus-like particle.

PS Disclosure; SEQ ID NO 11; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (Prp) or its dimer, or a Prp peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob disease. The present sequence is the amino acid sequence of a coat protein from a bacteriophage which may be used during the creation of the vaccine composition of the invention.

CC Sequence 329 AA;

Query Match 100.0%; Score 1749; DB 7; Length 329;

Best Local Similarity 100.0%; Pred. No. 3e-171; Mismatches 0; Indels 0; Gaps 0;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKLETVTLGNIGKQKQTLVNPBGVNPVTNGVASTSQAGVPALEKRVTVSVQPSRRR 60

DB 1 MAKLETVTLGNIGKQKQTLVNPBGVNPVTNGVASTSQAGVPALEKRVTVSVQPSRRR 60

QY 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTEIAALLASP 120

DB 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTEIAALLASP 120

QY 121 LIIDAIDQNPAYWTLIAGGSGSKPDVPIPDPPGKGKTCPPAIVSLSEVYEP 180

DB 121 LIIDAIDQNPAYWTLIAGGSGSKPDVPIPDPPGKGKTCPPAIVSLSEVYEP 180

QY 121 LIIDAIDQNPAYWTLIAGGSGSKPDVPIPDPPGKGKTCPPAIVSLSEVYEP 180

DB 181 PTKNRPPPIYNVAVELQPREFDVALKDLGNTKWRWDSRLSYTTFRCGNGYIDLDATY 240

QY 181 PTKNRPPPIYNVAVELQPREFDVALKDLGNTKWRWDSRLSYTTFRCGNGYIDLDATY 240

QY 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

DB 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

QY 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

DB 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-44130/41.

XX New compositions comprising a core particle and at least one antigen or PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies.

PS Disclosure; SEQ ID NO 11; 222pp; English.

XX The invention relates to a composition comprising a core particle having at least one first attachment site, and at least one antigen or antigenic determinant having at least one second attachment site. The antigen or antigenic determinant is a RANKL protein, RANKL fragment or RANKL peptide. The second attachment site is (non-) naturally occurring with the antigen or antigenic determinant, and is capable of association to the first attachment site. The antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful as a medicament, or for the manufacture of a medicament for treating bone diseases. The composition is especially useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies, and for stimulating mammalian immune system. This sequence represents a protein of the invention.

CC Sequence 329 AA;

Query Match 100.0%; Score 1749; DB 7; Length 329;

Best Local Similarity 100.0%; Pred. No. 3e-171; Mismatches 0; Indels 0; Gaps 0;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKLETVTLGNIGKQKQTLVNPBGVNPVTNGVASTSQAGVPALEKRVTVSVQPSRRR 60

DB 1 MAKLETVTLGNIGKQKQTLVNPBGVNPVTNGVASTSQAGVPALEKRVTVSVQPSRRR 60

QY 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTEIAALLASP 120

DB 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTEIAALLASP 120

QY 121 LIIDAIDQNPAYWTLIAGGSGSKPDVPIPDPPGKGKTCPPAIVSLSEVYEP 180

DB 121 LIIDAIDQNPAYWTLIAGGSGSKPDVPIPDPPGKGKTCPPAIVSLSEVYEP 180

QY 121 LIIDAIDQNPAYWTLIAGGSGSKPDVPIPDPPGKGKTCPPAIVSLSEVYEP 180

DB 181 PTKNRPPPIYNVAVELQPREFDVALKDLGNTKWRWDSRLSYTTFRCGNGYIDLDATY 240

QY 181 PTKNRPPPIYNVAVELQPREFDVALKDLGNTKWRWDSRLSYTTFRCGNGYIDLDATY 240

QY 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

DB 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

QY 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

DB 241 LATDQMRQKDIIEGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRP 300

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

QY 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

DB 301 SSGGAIPEDFTEKDKTCPIQAVIVPRA 329

XX OS unidentified.
XX PN WO2003040164-A2.
XX 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-EP012455.
XX PR 07-NOV-2001; 2001US-0331045P.
XX PR 18-JAN-2002; 2002US-00050902.
XX PR 21-JAN-2002; 2002WO-1B000166.
XX PR 19-JUL-2002; 2002US-0396636P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PI Bachmann M, Jennings G, Sonderegger I;
XX DR WPI, 2003-441518/41.
XX PT Composition comprising an ordered and repetitive antigen or antigenic
XX PT determinant array, useful as a medicament, or for manufacturing a
XX PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
XX PT Hodgkin's lymphoma.
XX PS Disclosure; SEQ ID NO 11; 245bp; English.
XX CC The invention relates to a composition comprising a virus-like particle
XX CC and at least one antigen, which is a protein or peptide of interleukin
XX CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
XX CC core particle with at least one first attachment site and at least one
XX CC antigen with at least one second attachment site, where the antigen is a
XX CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
XX CC is an attachment site naturally or not naturally occurring with the
XX CC antigen or antigenic determinant. The second attachment site is capable
XX CC of association to the first attachment site, and where the antigen or
XX CC antigenic determinant and the core particle interact through the
XX CC association to form an ordered and repetitive antigen array. The
XX CC compositions are useful as medicaments, or for manufacturing a medicament
XX CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
XX CC Hodgkin's lymphoma and related diseases. This sequence is used to
XX CC generate the compound of the invention.
XX SQ Sequence 329 AA;
Query Match 100.0%; Score 1749; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
DB 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
QY 61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRLTAALLASP 120
DB 61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRLTAALLASP 120
QY 121 LIIDAIDQINPXYWTLIIAGGSGSKPDVVPDPIDPPPGTGKTCPPAIVSLSEVYEP 180
DB 121 LIIDAIDQINPXYWTLIIAGGSGSKPDVVPDPIDPPPGTGKTCPPAIVSLSEVYEP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKRWMDSLSTTTRGCGNGYIDLDTY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKRWMDSLSTTTRGCGNGYIDLDTY 240
QY 241 LATDQAMDQKDYIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
DB 241 LATDQAMDQKDYIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTKDCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTKDCPIQAVIVPRA 329

RESULT 7
ADJ36301
ID ADJ36301 strand; protein; 329 AA.
XX AC ADJ36301;
XX DT 22-APR-2004 (first entry)
XX DE Bacteriophage Qbeta coat protein API protein subunit.
XX KW antiallergic; cytosatic; virucide; immunostimulant; vaccine;
XX KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
XX KW chronic disease; chronic viral disease; bacteriophage Qbeta;
XX KW coat protein; VLP; adjuvant; API coat protein.
XX OS Bacteriophage Qbeta.
XX PN WO2004000351-A1.
XX PD 31-DEC-2003.
XX PF 20-JUN-2003; 2003WO-EP006541.
XX PR 20-JUN-2002; 2002US-0389898P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PI Bachman MF, Renner WA;
XX DR WPI, 2004-108361/11.
XX CC New compositions comprising a virus-like particle (VLP), an
XX CC immunostimulatory substance bound to the VLP, and an antigen mixed with
XX CC the VLP, useful for enhancing immune response or for treating e.g. tumors
XX CC or chronic viral diseases.
XX PS Disclosure; SEQ ID NO 2; 252bp; English.
XX CC The invention describes a composition for enhancing an immune response in
XX CC an animal comprising a virus-like particle, an immunostimulatory
XX CC substance bound to the virus-like particle, and an antigen mixed with the
XX CC virus-like particle. The composition or the vaccine is useful in the
XX CC manufacture of a pharmaceutical for the treatment of a disorder or
XX CC disease such as allergies, tumours, chronic diseases and chronic viral
XX CC diseases. The composition is also useful for enhancing an immune response
XX CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
XX CC coat protein API protein subunit a virus like particle (VLP) that can be
XX CC used in the adjuvant of the invention.
XX SQ Sequence 329 AA;
Query Match 100.0%; Score 1749; DB 8; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
DB 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
QY 61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRLTAALLASP 120
DB 61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRLTAALLASP 120
QY 121 LIIDAIDQINPXYWTLIIAGGSGSKPDVVPDPIDPPPGTGKTCPPAIVSLSEVYEP 180
DB 121 LIIDAIDQINPXYWTLIIAGGSGSKPDVVPDPIDPPPGTGKTCPPAIVSLSEVYEP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKRWMDSLSTTTRGCGNGYIDLDTY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKRWMDSLSTTTRGCGNGYIDLDTY 240
QY 241 LATDQAMDQKDYIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
DB 241 LATDQAMDQKDYIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300

Db 241 LATDQAMRDQKYDIRGKKPGAFGNIERIYLSKINAYCSLSIDIAAYHADVIGFWRDP 300
QY 301 SSGGAIPEPDTFKDKCP1QAVIVPRA 329
Db 301 SSGGAIPEPDTFKDKCP1QAVIVPRA 329

RESULT 8
AD67147
ID AD67147 standard; protein; 329 AA.
XX AD67147;
XX
XX 06-MAY-2004 (first entry)
XX
XX Bacteriophage Qbeta coat protein for antigen display array.
XX
XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
XX antigenic array.
XX Bacteriophage Qbeta.
XX WO2004009124-A2.
XX 29-JAN-2004.
XX 18-JUL-2003; 2003WO-EP007849.
XX 19-JUL-2002; 2002US-0396638P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Bachmann MF, Fulurija A;
XX WPI; 2004-132866/13.
XX
XX New composition comprising a core particle having a first attachment site
XX and an antigen or antigenic determinant which is a ghrelin or ghrelin
XX peptide having a second attachment site, useful for treating obesity.
XX
XX Claim 12; SEQ ID NO 5; 175pp; English.

The invention relates to a new composition comprising: (i) a core
XX particle with at least one first attachment site; and (ii) at least one
XX antigen or antigenic determinant with at least one second attachment
XX site, where the antigen or antigenic determinant is ghrelin or a ghrelin
XX peptide, and where the second attachment site being consisting of an
XX attachment site not naturally occurring with the antigen or antigenic
XX determinant and an attachment site naturally occurring with the antigen
XX or antigenic determinant, where the second attachment site is capable of
XX association to the first attachment site, and where the ghrelin or a
XX ghrelin peptide and the core particle interact through the association to
XX form an ordered and repetitive antigen array. The composition is useful
XX for treating obesity. The repetitive array may form part of a phage or
XX bacterial display array. This peptide corresponds to a Bacteriophage
XX Qbeta coat protein which can be used as part of the repetitive or antigenic
XX array.

XX Sequence 329 AA;
XX
XX Query Match 100.0%; Score 1749; DB 8; Length 329;
XX Best Local Similarity 100.0%; Pred. No. 3e-17;
XX Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKLETVLGNIGKQGLVLRGVNPTNGVASLSQAGAVPALERKRVTVSVSGSPRRN 60
Db 1 MAKLETVLGNIGKQGLVLRGVNPTNGVASLSQAGAVPALERKRVTVSVSGSPRRN 60
QY 61 KNYVQVQKIONPRACTANGSCDPSVTROAYADVFSTFOYSTDEERAFFVRLAAILASP 120
Db 61 KNYVQVQKIONPRACTANGSCDPSVTROAYADVFSTFOYSTDEERAFFVRLAAILASP 120

QY 121 LLIDALDQLNPAVYTLTLIAGSGSGSKDPVTPDPPIPPPETGKTKCPFAWSLEVEYR 180
Db 121 LLIDALDQLNPAVYTLTLIAGSGSGSKDPVTPDPPIPPPETGKTKCPFAWSLEVEYR 180
QY 181 PTKRPMPTVNAVELQPEEPVALKDLGNKMRDMSRLSYTFRGCRNGYIDLDTATY 240
Db 181 PTKRPMPTVNAVELQPEEPVALKDLGNKMRDMSRLSYTFRGCRNGYIDLDTATY 240
QY 241 LATDQAMRDQKYDIRGKKPGAFGNIERIYLSKINAYCSLSIDIAAYHADVIGFWRDP 300
Db 241 LATDQAMRDQKYDIRGKKPGAFGNIERIYLSKINAYCSLSIDIAAYHADVIGFWRDP 300
QY 301 SSGGAIPEPDTFKDKCP1QAVIVPRA 329
Db 301 SSGGAIPEPDTFKDKCP1QAVIVPRA 329

RESULT 9
ADK52181
ID ADK52181 standard; protein; 329 AA.
XX ADK52181;
XX
XX 20-MAY-2004 (first entry)
XX
XX Bacteriophage Qbeta coat protein A1.
XX
XX Bacteriophage Qbeta coat protein A1.
XX
XX Bacteriophage Qbeta coat protein A1.
XX
XX Bacteriophage Qbeta.
XX WO2004016282-A1.
XX 26-FEB-2004.
XX 18-JUL-2003; 2003WO-EP007864.
XX 19-JUL-2002; 2002US-0396638P.
XX 15-MAY-2003; 2003US-0470432P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX (NOVA) NOVARTIS PHARMA AG.
XX Bachmann MF, Tisot A, Ortman R, Lueoend R, Staufenbiel M;
XX Frey P;
XX WPI; 2004-203731/19.
XX
XX Composition comprising a core particle with at least one attachment site,
XX and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
XX such as Alzheimer's disease.
XX
XX Claim 12; SEQ ID NO 5; 184pp; English.

The invention describes a novel composition comprising a virus-like core
XX particle with at least one attachment site, and an antigenic amyloid beta
XX 1-6 peptide. The new composition comprises: a core particle with at least
XX one first attachment site; and at least one antigen or antigenic
XX determinant with at least one second attachment site, where the antigen
XX or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
XX second attachment site comprises: an attachment site not naturally
XX occurring with the antigen or antigenic determinant; or an attachment
XX site naturally occurring with the antigen or antigenic determinant. The
XX second attachment site is capable of association to the first attachment
XX site and the beta 1-6 peptide and the core particle interact through the
XX association to form an ordered and repetitive antigen array. The
XX composition is useful for the manufacture of a medicament for treating
XX Alzheimer's disease and related diseases. This is the amino acid sequence
XX of an RNA bacteriophage coat protein that can be used in the preparation
XX of the compositions and vaccines of the invention.

SO Sequence 329 AA; 100.0%; Score 1749; DB 8; Length 329;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGAVPALEKRVTVSVSPSRNR 60
DB 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGAVPALEKRVTVSVSPSRNR 60
QY 61 KNYKVQVYIIONPTACTANGSCDPSVTRQAVADVTSFYQYSTDEERAFVRETLAALLASP 120
DB 61 KNYKVQVYIIONPTACTANGSCDPSVTRQAVADVTSFYQYSTDEERAFVRETLAALLASP 120
QY 121 LLIDAIDOLNPAWYTLTLIAGGSGSKPDPVLPDPIDPPGKXTCPFAIWSLEVEYEP 180
DB 121 LLIDAIDOLNPAWYTLTLIAGGSGSKPDPVLPDPIDPPGKXTCPFAIWSLEVEYEP 180
QY 181 PTKRNPWPIYNAVELQPREFVALKDLGNTKWRDWSRLSYTFRGCRNGYIDLDAITY 240
DB 181 PTKRNPWPIYNAVELQPREFVALKDLGNTKWRDWSRLSYTFRGCRNGYIDLDAITY 240
QY 241 LATQAMBDQKDIREGKKPGAFGNIERFIYLSKINAYCSLSDIAAYHADVIVGFWMDP 300
DB 241 LATQAMBDQKDIREGKKPGAFGNIERFIYLSKINAYCSLSDIAAYHADVIVGFWMDP 300
QY 301 SSGAIPDPFTKFDKTKCPIQAVIVVPPRA 329
DB 301 SSGAIPDPFTKFDKTKCPIQAVIVVPPRA 329

RESULT 10
ABRS6440
ID ABR56440 standard; protein; 328 AA.
XX ABR56440;
AC ABR56440;
DT 23-OCT-2003 (revised)
DT 28-JUL-2003 (first entry)
XX
DE Bacteriophage Q-beta coat protein SEQ ID NO:11.
XX
KM Antigen presenting cell; ABC; immune response; virus like particle; VLP;
KM cytosolic; virucide; antibacterial; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KM antihypoid; antidiabetic; neuroprotective; nootropic; osteopathic;
KM antitumoric; antiarthritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.
XX
OS Bacteriophage Qbeta.
XX
PN WO2003024480-A2.
XX
PD 27-MAR-2003.
XX
PF 16-SEP-2002; 2002MO-IB004252.
XX
PR 14-SEP-2001; 2001US-0318967P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Storm T, Lechner F;
XX
DR WPI; 2003-363095/34.
XX
PT A composition, useful for enhancing an immune response against an antigen
PT or immunising or treating tumors or infectious diseases, e.g. viral
PT infections.
XX

PS Disclosure; Page 168-169; 243pp; English.
XX
CC The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
CC antihypoid, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antitumoric and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumours and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 328 AA;

Query Match 99.1%; Score 1733.5; DB 6; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.2e-169;
Matches 328; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGAVPALEKRVTVSVSPSRNR 60
DB 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGAVPALEKRVTVSVSPSRNR 60
QY 61 KNYKVQVYIIONPTACTANGSCDPSVTRQAVADVTSFYQYSTDEERAFVRETLAALLASP 120
DB 61 KNYKVQVYIIONPTACTANGSCDPSVTRQAVADVTSFYQYSTDEERAFVRETLAALLASP 120
QY 121 LLIDAIDOLNPAWYTLTLIAGGSGSKPDPVLPDPIDPPGKXTCPFAIWSLEVEYEP 180
DB 121 LLIDAIDOLNPAWYTLTLIAGGSGSKPDPVLPDPIDPPGKXTCPFAIWSLEVEYEP 179
QY 181 PTKRNPWPIYNAVELQPREFVALKDLGNTKWRDWSRLSYTFRGCRNGYIDLDAITY 240
DB 181 PTKRNPWPIYNAVELQPREFVALKDLGNTKWRDWSRLSYTFRGCRNGYIDLDAITY 239
QY 241 LATQAMBDQKDIREGKKPGAFGNIERFIYLSKINAYCSLSDIAAYHADVIVGFWMDP 300
DB 241 LATQAMBDQKDIREGKKPGAFGNIERFIYLSKINAYCSLSDIAAYHADVIVGFWMDP 299
QY 301 SSGAIPDPFTKFDKTKCPIQAVIVVPPRA 329
DB 301 SSGAIPDPFTKFDKTKCPIQAVIVVPPRA 328

RESULT 11
ABR44543
ID ABR44543 standard; protein; 328 AA.
XX ABR44543;
AC ABR44543;
DT 23-OCT-2003 (revised)
DT 25-JUL-2003 (first entry)
XX
DE Bacteriophage Q-beta coat protein SEQ ID NO:11.
XX
KM Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
KM hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
KM immunostimulant; cytosolic; antiallergic; virucide; antibacterial;

immune response; immunisation; allergy; tumour; breast cancer; neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles; chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

Bacteriophage Qbeta.

WO2003024481-A2.

27-MAR-2003.

16-SEP-2002; 2002WO-IB004132.

14-SEP-2001; 2001US-0318994P.

22-APR-2002; 2002US-0374145P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

(MAUR/) MAURER P.

(TIS/) TISSOT A.

(SCHW/) SCHWARZ K.

(MEIJ/) MEIJERINK E.

(LIP/) LIPOWSKY G.

(PUMP/) PUMPENS P.

(CIEL/) CIELENS I.

(RENN/) RENHOFA R.

Maurer P, Tisot A, Schwarz K, Meijerink E, Lipowsky G, Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T, WPI; 2003-354564/33.

New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.

Disclosure; Page 247-249; 322pp; English.

The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance. The immunostimulatory substance is bound to the VLP. Also described: (1) enhancing an immune response in an animal by introducing (C) into the animal; (2) producing (C) for enhancing an immune response in an animal; (3) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; and (4) immunising or treating an animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (c) boosting a T cell response in the animal by administering the vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and antibacterial activities. (1) can be used in vaccines for enhancing an immune response in an animal, particularly a B cell response, a T cell response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine comprising (C) can also be used for immunising or treating an animal, e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, reptiles or fish. (C) is particularly useful in prophylactic or therapeutic vaccines against allergies, tumors (e.g. breast cancer, neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis, measles or chicken pox), or bacterial infections (e.g. tuberculosis, pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612 represent sequences used in the exemplification of the present invention. (Updated on 23-OCT-2003 to standardise OS field)

Sequence 328 AA:

Query Match 99.1%; Score 1733.5; DB 6; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.2e-169; Indels 1; Gaps 1;
Matches 328; Conservative 0; Mismatches 0;

1 MAKLEVTTLNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQSPSRNR 60
1 MALEVTTLNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQSPSRNR 60
61 KNYKVQVYKIONPTACTANGSCDBSVTRQAVADVTFSTQYSTDERAFVTEIALALASP 120

|||||
61 KNYKVQVYKIONPTACTANGSCDBSVTRQAVADVTFSTQYSTDERAFVTEIALALASP 120
121 LLIDAIQDLPNAYMTLLIAGGSSGSKDPVPYDPDPPIPPPGTGYCPFAIWSLEVEYEP 180
121 LLIDAIQDLPNAYMTLLIAGGSSGSKDPVPYDPDPPIPPPGTGYCPFAIWSLEVEYEP 179
181 PTKRPMPIYNAVELQPREPVALKDLIGNTKMDWDSRLSYTFRGCRNGYIDLDAITY 240
180 PTKRPMPIYNAVELQPREPVALKDLIGNTKMDWDSRLSYTFRGCRNGYIDLDAITY 239
241 LATDQAMRDQKDYDREGKPPAFGNIRFYLKLSINAYCSLSDIAAAYADGVYIGFMRDP 300
240 LATDQAMRDQKDYDREGKPPAFGNIRFYLKLSINAYCSLSDIAAAYADGVYIGFMRDP 299
301 SSGAIPDPFTKPKPCPIQAVIWPRA 329
300 SSGAIPDPFTKPKPCPIQAVIWPRA 328

RESULT 12

ABR56445
ID ABR56445 standard; protein; 329 AA.

ABR56445;

28-JUL-2003 (first entry)

Bacteriophage SP coat protein SEQ ID NO:16.

Antigen presenting cell; APC; immune response; virus like particle; VLP; cytostatic; virucide; antibacterial; antiparasitic; fungicide; antiallergic; immunosuppressive; antiaddictive; antiinflammatory; antihypoid; antidiabetic; neuroprotective; nootropic; osteopathic; antirheumatic; antiarthritic; vaccine; immunisation; infectious disease; anti-viral protection; tumour; allergy; drug addiction; Crohn's disease; graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis; Alzheimer's disease; osteoporosis; rheumatoid arthritis;

Bacteriophage SP.

WO2003024480-A2.

27-MAR-2003.

16-SEP-2002; 2002WO-IB004252.

14-SEP-2001; 2001US-0318967P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

Bachmann MF, Storni T, Lechner F;

WPI; 2003-363095/34.

A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, or immunizing or treating tumors or infectious diseases, e.g. viral infections.

Disclosure; Page 173-174; 243pp; English.

The present invention describes a composition (C) for enhancing an immune response against an antigen or a virus-like particle in an animal. (C) comprises a virus-like particle (VLP) bound to at least one antigen, or a VLP capable of being recognised by the immune system of the animal. (C) described: (1) enhancing an immune response against an antigen or a VLP in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral

protection in an animal comprising introducing (C) into the animal. (C) has cytotoxic, virucide, antibacterial, antiparasitic, fungicide, antifungal, immunosuppressive, antidiabetic, antitubercular, antitumor, antihypertensive, neuroprotective, nootropic, osteopathic, antirheumatic and antidiabetic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunizing or treating tumors and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69832 to ACC69852 and ABR56401 to ABR56509 represent sequences used in the exemplification of the present invention

Sequence 329 AA;

Query Match 55.9%; Score 978; DB 6; Length 329;
Best Local Similarity 58.3%; Pred. No. 9.9e-92;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

2 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVAGSISQAGAVPALEKRVTVSVSOPSRRNK 61
1 AKLNVTLSTKIGKNDQTLTPRGVNPNGVAGSISQAGAVPALEKRVTVSVSOPSRRNK 60
62 NYKVQKIQNPACTANGSCDPSVTRQAYADVTFFQYSTDEBAFVTELAALLASPL 121
61 NKVQIKIQNPACTCRD-ACDPSVTRSAFADVTLSYSTDEBALRTELAALLADPL 119
122 LIDAIIDOLNPAYW-TLLIAGGGSGSKPD---PVLPDPIDPPPGTKTCFPAIWSLEE 176
120 IVDADININPAMWALLVASSGGGNDPDPVPVVPD--VKPPDGTGRKCFACRYLGS 177
177 VYEPPTKRPMPWYINAVELQPREFDVALKDLGNTKMDMSRLS---YTFRRGCRNGY 233
178 IYEVGKESGP-DIYERGDEVSVTFDYALEDFGNTMKNMDRLSDYDANRRRCRNGY 236
234 IDLDATYIATDQAMDDQKDIRGKKPGAFGNIEFTYLSKSI--NAYCSISDIAYVHADG 291
237 IDLDATAMQSDDFVLSGRGVAKVFPAGFSGIK---YLLNTOGAMWLDLSEVTAYRSYG 293
292 VIVGFWRPDSSGGAIPFDFTKDKTKCPIQAVIIVP 327
294 NVIGFWTD-SKSPOLPTDFTQNSANCPVQTVIIR 328

RESULT 13

ABR44548 standard; protein; 329 AA.

ABR44548;

25-JUL-2003 (first entry)

Bacteriophage SP coat protein SEQ ID NO:16.

Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV; hepatitis B virus; lymphocytic choriomeningitis virus; vaccine; immunostimulant; cytotoxic; antiallergic; virucide; antibacterial; immune response; immunization; allergy; tumor; breast cancer; neuroblastoma; leukemia; viral disease; influenza; hepatitis; measles; chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

Bacteriophage SP.

WO2003024481-A2.

27-MAR-2003.

16-SEP-2002; 2002WO-IB004132.

14-SEP-2001; 2001US-0318994P.

22-APR-2002; 2002US-0374145P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.
MAURER P.
TISSOT A.
SCHWARTZ K.
MEIJERINK E.
LITPOWSKY G.
PUMPERTS P.
CIELENS I.
REINHOLD R.
Maurer P, Tissot A, Schwartz K, Meijerink E, Litpowsky G, PumPERTS P, Cielens I, Reinholt R, Bachmann MF, Storni T; MPI; 2003-354564/33.

New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.

Disclosure; Page 252-253; 322pp; English.

The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance. The immunostimulatory substance is bound to the VLP. Also described: (1) enhancing an immune response in an animal by introducing (C) into the animal; (2) producing (C) for enhancing an immune response in an animal; (3) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; and (4) immunizing or treating an animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (c) boosting a T cell response in the animal by administering the vaccine. (C) has immunostimulant, cytotoxic, antiallergic, virucide and antibacterial activities. (1) can be used in vaccines for enhancing an immune response in an animal, particularly a mammal or human. Specifically, (C) is useful for enhancing a B cell response, a T cell response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine comprising (C) can also be used for immunizing or treating an animal, e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, reptiles or fish. (C) is particularly useful in prophylactic or therapeutic vaccines against allergies, tumors (e.g. breast cancers, neuroblastoma, or leukemia), viral diseases (e.g. influenza, hepatitis, measles or chicken pox), or bacterial infections (e.g. tuberculosis, CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44512 represent sequences used in the exemplification of the present invention

Sequence 329 AA;

Query Match 55.9%; Score 978; DB 6; Length 329;
Best Local Similarity 58.3%; Pred. No. 9.9e-92;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

2 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVAGSISQAGAVPALEKRVTVSVSOPSRRNK 61
1 AKLNVTLSTKIGKNDQTLTPRGVNPNGVAGSISQAGAVPALEKRVTVSVSOPSRRNK 60
62 NYKVQKIQNPACTANGSCDPSVTRQAYADVTFFQYSTDEBAFVTELAALLASPL 121
61 NKVQIKIQNPACTCRD-ACDPSVTRSAFADVTLSYSTDEBALRTELAALLADPL 119
122 LIDAIIDOLNPAYW-TLLIAGGGSGSKPD---PVLPDPIDPPPGTKTCFPAIWSLEE 176
120 IVDADININPAMWALLVASSGGGNDPDPVPVVPD--VKPPDGTGRKCFACRYLGS 177
177 VYEPPTKRPMPWYINAVELQPREFDVALKDLGNTKMDMSRLS---YTFRRGCRNGY 233
178 IYEVGKESGP-DIYERGDEVSVTFDYALEDFGNTMKNMDRLSDYDANRRRCRNGY 236
234 IDLDATYIATDQAMDDQKDIRGKKPGAFGNIEFTYLSKSI--NAYCSISDIAYVHADG 291
237 IDLDATAMQSDDFVLSGRGVAKVFPAGFSGIK---YLLNTOGAMWLDLSEVTAYRSYG 293

QY 292 VIVGFWRDPSGGAIPFDFTKFCPCPQAVIWP 327
 DB 294 MWIGFWTD-SKSPQLPTDFTQNSANCPCVQYIIITP 328

RESULT 14
 ID ADD24123 standard; protein; 329 AA.

AC ADD24123;

DE 15-JAN-2004 (first entry)

DE Bacteriophage SP coat protein A1.

KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; coat protein.

OS Bacteriophage SP.

PN W02003059386-A2.

PD 24-JUL-2003.

PF 17-JAN-2003; 2003WO-EP000460.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 08-JUL-2002; 2002US-0393725P.

PR 18-JUL-2002; 2002US-0396590P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Pellizzoli E, Renner WA;

XX WPI; 2003-598483/56.

PT A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprising a virus-like particle (e.g. RNA-
 PT phase) and at least one prion protein or peptide bound to the virus-like
 PT particle.

PS Disclosure; SEQ ID NO 16; 246bp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)

CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the

CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament

CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob

CC Disease. The present sequence is the amino acid sequence of a coat
 CC protein from a bacteriophage which may be used during the creation of the

CC vaccine composition of the invention.

XX Sequence 329 AA;

Query Match 55.9%; Score 978; DB 7; Length 329;

Best Local Similarity 58.3%; Pred. No. 9.9e-97; Indels 18; Gaps 9;

Matches 196; Conservative 45; Mismatches 77;

QY 2 AKLETVTLLGNIGKDGKQTLVIMRGVNPITGVASLSGAGVPALEKRVTVSVSOPSNRK 61

DB 1 AKLNQVTLSTKIGKNGDQTLVTPRGVNPITGVASLSGAGVPALEKRVTVSVSOPSNRK 60

QY 62 NYKYQVQIONPTACTANGSCDPSVTRQAVYADVTFSPFYQYSTDERRARVRIELALLASPL 121

DB 61 NFKVQIKLQNPVACTRD-ACDPVTRSAFADVTLSTFSYSTDERRALRIETELALLADPL 119

QY 122 LIDAIDQINPAW-TLIANGSGSGSKPD----PIIPPEPIDPPEGKTYTCCPAIWSLEE 176
 DB 120 IVDALDINLNPAYMALVAVSSGGGDNFEDPDVVPVDP--VKPDPDGTGRYKCPFCACYRIGS 177

QY 177 VYEPPTKNRPWPIYNAVELQREFDVALKDLGNTKPRDMDSRLS---YTFPRGGRNGY 233

DB 178 IYEVKEGESP-DYERGEVSVTFDYALEDFLGNTNMNMWQRLSDVDIANRRRCRGNGY 236

QY 234 IDLDATYATQAMKDYDIREGKPGAFGNIERFIYLSKI--NAYCSLSDIAYHADG 291

DB 237 IDLDATNAQSDDFVLSGRYGRKRVKFPFAGFSIK---YLNIQGDAMLDSEVAYRBYG 293

QY 292 VIVGFWRDPSGGAIPFDFTKFCPCPQAVIWP 327

DB 294 MWIGFWTD-SKSPQLPTDFTQNSANCPCVQYIIITP 328

RESULT 15

ID ADJ82049 standard; protein; 329 AA.

AC ADJ82049;

DE 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 KW bone disease; encephalopathy; immune system stimulation.

OS Unidentified.

PN W02003039225-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012449.

PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-441430/41.

PT New compositions comprising a core particle and at least one antigen or
 PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 PT of bone diseases, particularly mammalian encephalopathies.

PS Disclosure; SEQ ID NO 16; 222bp; English.

XX The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic

CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL

CC peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to

CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and

CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The

CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.

XX Sequence 329 AA;

Query Match 55.9%; Score 978; DB 7; Length 329;
Best Local Similarity 58.3%; Pred. No. 9.9e-92;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

```
QY 2 AKLEVTYTLGNIGKDGKQTLVLPNGVNPNGVNSISQAGAVPALERKVTVSOSPRNK 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 AKLNQVTLKIGKNGDQTLTPRGVNPNGVNSISQAGAVPALERKVTVSVAQPSRNK 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 NKVQVKIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDERAFVTELAALLASPL 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 NFKVQIKIQNPACTRD-ACDPSVTRSAFADYTLSTSYSTDERALIRTELAALLADPL 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 LIDALDQNPAYW-TLLINGGGSGSKPD---PVLPDPIDPPPGTKYTCPPAIIWSLEE 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 120 IVDALDINPAYMALLVASSGGDNPSDDPVVVPD--VKPPDGTGRYKCFACRYLGS 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 VVEPPTKRNPPFIYNAVELQPREFDVALKDLGNTKWRDMSRLS---YTFRGCRNGY 233
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 178 IYEVGKESGP-DIERGDEVSVTFDIALDFLGNTNWRMDQRLSDYDIANRRRCRNGY 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 234 IDLDATYLATDQMRDQKYDIREGKKPGAFGNIERFIYLSI--NAYCSLSDIAAYHADG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 237 IDLDATANGSDDFVLSGRGVAKVKEPGAFSGIK---YLANIQGDAMLDLSEVTAYRSYG 293
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 292 VIVGFWRDPSGGAIIPDFTKFDKTKCPIQAVIIVP 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 294 MVIGFWTD-SKSPQLPTDFTQFNANCPVQTVIITP 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: January 4, 2005, 09:10:59
Job time : 99.9054 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 25.8269 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-4
Perfect score: 1749
Sequence: 1 MAKLETVLGNIGKDKQTL.....FTKPKTKCPQIVIVPRA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues
Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	5.5	1426	3	US-09-136-574A-43
2	95.5	5.5	1326	4	US-09-252-991A-17932
3	94	5.4	401	3	US-08-289-222B-3
4	94	5.4	401	2	US-09-054-526B-3
5	94	5.4	501	2	US-08-288-508C-2
6	94	5.4	501	4	US-08-981-490B-1
7	94	5.4	501	4	US-09-386-450D-2
8	91.5	5.2	920	4	US-09-463-402-6
9	91	5.2	1509	4	US-09-410-551B-23
10	91	5.2	1509	4	US-09-940-316B-23
11	90	5.1	495	1	US-08-455-559-10
12	90	5.1	495	1	US-09-145-060-10
13	90	5.1	495	3	PCT-US94-00657-10
14	90	5.1	1569	4	US-09-711-164-312
15	89.5	5.1	626	4	US-09-485-717-2
16	89.5	5.1	626	4	US-09-948-722-2
17	88.5	5.1	2972	3	US-09-579-181-2
18	88.5	5.1	3118	3	US-09-579-181-1
19	87	5.0	278	2	US-08-160-524A-4
20	87	5.0	283	2	US-08-160-524A-2
21	86.5	4.9	561	4	US-09-248-796A-18959
22	86	4.9	528	2	US-08-466-589-2
23	86	4.9	528	2	US-08-700-636-2
24	86	4.9	528	3	US-08-467-574-2
25	86	4.9	528	3	US-09-217-345-2
26	86	4.9	528	4	US-09-892-985-2
27	86	4.9	933	3	US-08-293-728-2

28	86	4.9	933	3	US-09-421-868-2	Sequence 2, Appl1
29	86	4.9	936	4	US-08-956-171E-5249	Sequence 5249, Ap
30	86	4.9	936	4	US-08-781-986A-5249	Sequence 5249, Ap
31	86	4.9	1651	3	US-09-540-245A-18	Sequence 18, Appl
32	85.5	4.9	312	1	US-08-414-625-2	Sequence 2, Appl1
33	84.5	4.8	1154	4	US-09-134-000C-6122	Sequence 6122, Ap
34	84	4.8	1469	4	US-09-262-537-58	Sequence 58, Appl
35	84	4.8	1577	2	US-08-793-824-2	Sequence 2, Appl1
36	83.5	4.8	415	4	US-09-252-991A-29602	Sequence 29602, A
37	82.5	4.7	695	1	US-08-164-839-8	Sequence 8, Appl1
38	82.5	4.7	695	1	US-08-583-799-8	Sequence 8, Appl1
39	82.5	4.7	696	1	US-08-164-839-10	Sequence 10, Appl
40	82.5	4.7	696	1	US-08-583-799-10	Sequence 10, Appl
41	82	4.7	148	4	US-09-270-767-42039	Sequence 42039, A
42	82	4.7	409	4	US-09-328-352-4249	Sequence 4249, Ap
43	82	4.7	842	4	US-08-591-502B-50	Sequence 50, Appl
44	82	4.7	842	4	US-08-591-502B-51	Sequence 51, Appl
45	82	4.7	982	4	US-09-556-877-176	Sequence 176, App

ALIGNMENTS

RESULT 1
US-09-136-574A-43
Sequence 43, Application US/09136574A
Patent No. 6294366
GENERAL INFORMATION:
APPLICANT: Farrington, Graham K.
Anderson, Paige
Gibbs, Moreland
Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for Treating Cellulose Containing Fabrics Using Truncated Cellulase Enzyme Compositions
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/9932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6294366
SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-136-574A-43

Query Match 5.5%; Score 97; DB 3; Length 1426;
Best Local Similarity 21.2%; Pred. No. 0.65;
Matches 80; Conservative 44; Mismatches 156; Indels 98; Gaps 20;

QY 22 LMRGPNPNNGVASSLSQAG---AVPALERKRVTVSOSPSSRRKRYKVQVKNPACTA 77
DB 240 LKSKGV-PIHIGIQMOSHINWNPVSSEINISIKLFSSTIGIEIHITELMSLYN-XGSNE 297
QY 78 NGSCDPS--VTRQA--YADVTFSTQYS---TDEERAFVTELAALLAS-----PLTIDA 125
DB 298 NYSTPPQDILQRAQKXKDIFTMLRKRYKGIYVCTVFWGKDDYSLNSSSKDWPFLFPD 357
QY 126 IDQLNPAYWTLIAGGSGSKDPVVPDPPIPP-----PRTGKRYTGP 168
DB 358 DYSAKPAYSVLEAAGASAS-PSPTVATAPPTPTPTVATPTPTPTPTPTPTGSGS---- 412
QY 169 FAIWSLEVEYEPPTKN-----RPMPIYNAVELQPREFDVALKDLGNTKMDW-- 216
DB 413 ---GKLVLY---KNNETSASTGSRPM--FKIYNGSSSDV-----LSRYKIRYWT 456
QY 217 -DSRLSYTFRGCGRGXYIDLDAVTLATQAMRDQKDYIREGKPGA----- 262
DB 457 VDDKXQSANCDMAQIGASVTFNFVKLSGVSAGADYILEVGFSSGAGLOPKDAGDIO 516
QY 263 -----FNIERTIYKSLINAVCSLDIAVADGYVGFV-RDPSSGAIFFDPT 311
DB 517 VRFNKDMSVYNQADMSWISMTDYGEMAKVLY-VDGVLV--WGOEP--GGATAPAPTA 571
QY 312 KFDKTKCPIDAVIVPRA 329
DB 572 TATPTPTPTATVPTPTPA 589

RESULT 2
US-09-252-991A-17932

; Sequence 17932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17932
; LENGTH: 1326
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17932

Query Match 5.5%; Score 95.5; DB 4; Length 1326;
Best Local Similarity 24.9%; Pred. No. 0.84; Indels 105; Gaps 25;
Matches 92; Conservative 48; Mismatches 124;

QY 17 KOTLVNPRG---VNPTNGVASLSQAGAVPALEKRVTVSOPSSRRKRYKVQ-VKICN 71
DB 338 EQQKIFQPRPKRVKLVSLN-VAEISL--TVGIGIYVIDSGARISRYSAKQVRLPIEA 394
QY 72 PTACTAN-----GSCDPSVTRQAYADVTFSTQYS---TDEERAFVTELAALLASPLI-- 122
DB 395 VSQASANQRKRCRVERGICVRLYSEDFNARAPAFDPE--IRTNLAIVIIQMLRL 452
QY 123 --TDAIDQANA-----VTTLL--IAGGSGSKDPV--IDPPIDPPG----- 161
DB 453 GDIEAFPIEPPDKAIKDGFTLLQELSAVNRGOLTPLGQRLALPLIDPLGMLLEAA 512

QY 162 -TGKTCFPAIWSLEVEYEPPTKNRPMPIYNAVELQ-PREFDVALKDL--GNTKMDW 217
DB 513 QQG-----SLEEVLY-----TVASALSVDPRERPERVROQADQAHQWDPD 554
QY 218 SRLS--YTPFGG-----CRGN--GYIDL-----DA-----TYLATDQAM-- 247
DB 555 SDFAALINLMGFEERQALGNSALRSWCRCRNFILYRLKEWRRAHROLTLICRELKLPF 614
QY 248 -RDKYDIREBK-RPGAFNIERTF-----YLSINAYCS--LSDIAVHADGVIVG----- 295
DB 615 GRPAKAEKKEAKKAGSADNREVPGLDYAAVHKAILLSGLISQIGKAEKSGDYLGAQR 674
QY 296 -FWRDPSG 303
DB 675 RFWHPSSG 683

RESULT 3
US-08-289-222E-3

; Sequence 3, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-289-222E-3

Query Match 5.4%; Score 94; DB 3; Length 401;
Best Local Similarity 21.7%; Pred. No. 0.18;
Matches 77; Conservative 35; Mismatches 115; Indels 128; Gaps 18;

QY 22 LNPRGVNTNVAASLSQGANVP-----ALEKRTVSVSQSR----- 58
DB 22 VTPKQQLP--GKAPPKAGSVSSFLKKAREPGPREPKEFRPPPTTPHEMYLSLYRT 79
QY 59 ---NRKNYKVQVKIONPACTANGSCD-----PSYTRQAYV-DYTFSTQYSTDEER 106
DB 80 LSDADRKGNSSVKLEAGLANTITSFDKQDDRGFPVVRKQRYVFDI-----SALEKD 132
QY 107 AFVTELTALLASPLLDALDQNPAYWTLIAGG-----SGSKDPVPIPPPP 155
DB 133 GLGAEHLRLRKPF-----SDTAKPA-----APGGRAAQLKSSCPSGRQASLLDVRS 182
QY 156 IDPPPGTKYTCPPAIVNSLEVEYEPPTKX-----RPWLYNAVELOPREFDVALKD- 206
DB 183 VPGLDGSGMEV--FDIWLKFRNF---KNSAQLCLELAWERGRAVDLRGLGFDRAARQV 236
QY 207 -----LLGNTKWDMDWSRLSYTTFRGGRNGYIDLAT---YATPOAMBDQYDIRE 256
DB 237 HEKALFLVFGRTKRD---LFFNEIKARSGOD---DKTYVEYLFSGRRKRRAPLATRQ 288
QY 257 GKKGAPFNIRFRIFYLKSINAYCSLS-----DIAYHADGV 292
DB 289 GKRPS-----KYLKARCSRKALHVNFKQMGWMDWIIAPLEYEAFHCEGL 332

RESULT 4
US-09-054-526B-3
Sequence 3, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TITEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, MONICA CHIN
REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-3

Query Match 5.4%; Score 94; DB 3; Length 401;
Best Local Similarity 21.7%; Pred. No. 0.18;
Matches 77; Conservative 35; Mismatches 115; Indels 128; Gaps 18;

QY 22 LNPRGVNTNVAASLSQGANVP-----ALEKRTVSVSQSR----- 58
DB 22 VTPKQQLP--GKAPPKAGSVSSFLKKAREPGPREPKEFRPPPTTPHEMYLSLYRT 79
QY 59 ---NRKNYKVQVKIONPACTANGSCD-----PSYTRQAYV-DYTFSTQYSTDEER 106
DB 80 LSDADRKGNSSVKLEAGLANTITSFDKQDDRGFPVVRKQRYVFDI-----SALEKD 132
QY 107 AFVTELTALLASPLLDALDQNPAYWTLIAGG-----SGSKDPVPIPPPP 155
DB 133 GLGAEHLRLRKPF-----SDTAKPA-----APGGRAAQLKSSCPSGRQASLLDVRS 182
QY 156 IDPPPGTKYTCPPAIVNSLEVEYEPPTKX-----RPWLYNAVELOPREFDVALKD- 206
DB 183 VPGLDGSGMEV--FDIWLKFRNF---KNSAQLCLELAWERGRAVDLRGLGFDRAARQV 236
QY 207 -----LLGNTKWDMDWSRLSYTTFRGGRNGYIDLAT---YATPOAMBDQYDIRE 256
DB 237 HEKALFLVFGRTKRD---LFFNEIKARSGOD---DKTYVEYLFSGRRKRRAPLATRQ 288
QY 257 GKKGAPFNIRFRIFYLKSINAYCSLS-----DIAYHADGV 292
DB 289 GKRPS-----KYLKARCSRKALHVNFKQMGWMDWIIAPLEYEAFHCEGL 332

RESULT 5
US-08-288-508C-2
Sequence 2, Application US/08288508C
Patent No. 5994094
GENERAL INFORMATION:
APPLICANT: H titen, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
TITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaïdo, Marmelestein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,508C
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 26 829.3
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 18 222.8
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 157.5
FILING DATE: 09-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: P-41,092
REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-508C-2

Query Match 5.4%; Score 94; DB 2; Length 501;
Best Local Similarity 21.7%; Pred. No. 0.26; Mismatches 115; Indels 128; Gaps 18;
Matches 77; Conservative 35;

QY 22 LNPRGVNPTNGVASISQAGAVP-----ALEKRVTVSVSQPSR----- 58
DB 122 VTPKQGLP--GGKAPPKAGSVSSFLKKAREGPPREKEPPRPPIPTPHEMYMLSLYRT 179
QY 59 ----NRKNYKVOVKIQNPACTANGSCD-----PSVTRQAYV-DVTFSTFOYSTDEER 106
DB 180 LSDADRKGGNSSVKLEAGLANITTSFIDKGDDRGVVRKQRYVEDI-----SALEKD 232
QY 107 AFVRETELAAVLASPLLIDALDQNPAYWTLTLAGG-----SGSKDPVYIDPP 155
DB 233 GLIGAEHLRLIRKKP-----SDTAKPA-----APGGRAAQLKSSCPSGRQPSASLIDVRS 282
QY 156 IDPPPTGKYTCPPFAIWSLEEVYEPPTKN-----RPMPIYNAVELQPREPVALKD- 206
DB 283 VGLDGSQGEV--FDIWKLFNRP-----KNSAQCLELAMEGRVAVDLGLGFDRAARQV 336
QY 207 -----LIGNTYKMDWSRLSYTTPRCGRNGYIDLDT--YATDQAMPDQKTDIRE 256
DB 337 HEKALFLVFGRTKKRD-----LFENEIKARSGD--DRTVVEYLFSGRRKRRAPLATQ 388
QY 257 GKKGAFGNIERFIYLSINAYCSLS-----DIAAYHADGV 292
DB 389 GRKPS-----KNLKAQCSRKALHVNFKMGMDMTIAPLEYEAFHCEGL 432

RESULT 6

US-08-981-490B-1
Sequence 1, Application US/08981490B
Patent No. 6531450
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B
CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE/195 25 416.3
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 501
TYPE: PRT

ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match 5.4%; Score 94; DB 4; Length 501;
Best Local Similarity 21.7%; Pred. No. 0.26; Mismatches 115; Indels 128; Gaps 18;
Matches 77; Conservative 35;

QY 22 LNPRGVNPTNGVASISQAGAVP-----ALEKRVTVSVSQPSR----- 58
DB 122 VTPKQGLP--GGKAPPKAGSVSSFLKKAREGPPREKEPPRPPIPTPHEMYMLSLYRT 179
QY 59 ----NRKNYKVOVKIQNPACTANGSCD-----PSVTRQAYV-DVTFSTFOYSTDEER 106
DB 180 LSDADRKGGNSSVKLEAGLANITTSFIDKGDDRGVVRKQRYVEDI-----SALEKD 232
QY 107 AFVRETELAAVLASPLLIDALDQNPAYWTLTLAGG-----SGSKDPVYIDPP 155
DB 233 GLIGAEHLRLIRKKP-----SDTAKPA-----APGGRAAQLKSSCPSGRQPSASLIDVRS 282
QY 156 IDPPPTGKYTCPPFAIWSLEEVYEPPTKN-----RPMPIYNAVELQPREPVALKD- 206
DB 283 VGLDGSQGEV--FDIWKLFNRP-----KNSAQCLELAMEGRVAVDLGLGFDRAARQV 336
QY 207 -----LIGNTYKMDWSRLSYTTPRCGRNGYIDLDT--YATDQAMPDQKTDIRE 256
DB 337 HEKALFLVFGRTKKRD-----LFENEIKARSGD--DRTVVEYLFSGRRKRRAPLATQ 388
QY 257 GKKGAFGNIERFIYLSINAYCSLS-----DIAAYHADGV 292
DB 389 GRKPS-----KNLKAQCSRKALHVNFKMGMDMTIAPLEYEAFHCEGL 432

RESULT 7

US-09-386-450D-2
Sequence 2, Application US/09386450D
Patent No. 6764994
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-? Family
FILE REFERENCE: 100564-09022
CURRENT APPLICATION NUMBER: US/09/386,450D
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: US 08/288,508
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: DE P 43 26 829.3
PRIOR FILING DATE: 1993-08-10
PRIOR APPLICATION NUMBER: DE P 44 18 222.8
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: DE P 44 20 157.5
PRIOR FILING DATE: 1994-06-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(501)
OTHER INFORMATION: TGF-beta protein MP-52 precursor
US-09-386-450D-2

Query Match 5.4%; Score 94; DB 4; Length 501;
Best Local Similarity 21.7%; Pred. No. 0.26; Mismatches 115; Indels 128; Gaps 18;
Matches 77; Conservative 35;

QY 22 LNPRGVNPTNGVASISQAGAVP-----ALEKRVTVSVSQPSR----- 58
DB 122 VTPKQGLP--GGKAPPKAGSVSSFLKKAREGPPREKEPPRPPIPTPHEMYMLSLYRT 179
QY 59 ----NRKNYKVOVKIQNPACTANGSCD-----PSVTRQAYV-DVTFSTFOYSTDEER 106

Db 180 LSDADRGKGNSSVKLEAGLANTTTSFIDGQDGRGVKRVFDI-----SLEKED 232
Qy 107 AFVETELALLASPLILDAIDOLNPAWTLIAGG-----SSKDPVPIDPP 155
Db 233 GLGAEELRLRKPP-----SDTRAKP-----APGGRAQLKSSGSPGRQPSLIDVVS 282
Qy 156 IDPPGTGKYTCPPAIVSLSEVEEPEPTKQ-----RPMPIYNAVELQPREVDALKD- 206
Db 283 VGLDGSQGWV--FDIWKLFRRF-----KNSAQCLELEAMERGRAVDLRLGDFDRARQV 336
Qy 207 -----LLGNKRWDMDSRLSYTTRGCGNGYIDLDT---YLATDQAMDQKTDIE 256
Db 337 HEKALFLVFGRTKRD---LFEENEIKARSGOD---DKTYVEYLFSGRRKRRAPLATQ 388
Qy 257 GKGPAGNIRFFIYLSINAYCSLS-----DIAVYHADGV 292
Db 389 GKRPS-----KNLKARCSKALHVNKDKMDMDIAPLEYEAFHCEGL 432

RESULT 8
US-09-463-402-6

Sequence 6, Application US/09463402
Patent No. 6586510
GENERAL INFORMATION:
APPLICANT: Lubitz, Werner
APPLICANT: Resch, Stephanie
TITLE OF INVENTION: Secretion of Carrier-bound Proteins into the Periplasm
FILE REFERENCE: 05649059
CURRENT APPLICATION NUMBER: US/09/463,402
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: DE19732829.6
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: PCT/EP98/04723
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 920
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-463-402-6

Query Match 5.2%; Score 91.5; DB 4; Length 920;
Best Local Similarity 21.5%; Pred. No. 1.3;
Matches 64; Conservative 40; Mismatches 87; Indels 107; Gaps 15;

Qy 55 QPSNRKRYKQVKIQNPTACTANGSCDPSVTRQAVADYTFSP----- 97
Db 4 QPKSYRK-----FVATTATPAWVASAVAVSAASFTDVAPOYKALIDFLVSTGATKGT 58
Qy 98 -TQYTDERARAVRTBLALLASPLILDAIDOLNPAWTL-----LIAGGSG 144
Db 59 ETKFQVYDE--ITRIDAAVILARVKTLD--VDNAKAGFDVPRAKYVNAIVEGVLNG 115
Qy 145 SKPDVPIPDPPGTGKYTCPPAIVSLSEVEEPEPTKQRPMPYNAVELQPREVDAL 204
Db 116 KAP-----GKF-----GATDPLR-----VEM-----A 133
Qy 205 KDLGNTRWDMDSRLSYTTRGCGNGYIDLATYATDQAMDQKTDIREGKPP--G 261
Db 134 KLIARRYKLKADVDLQLPFT-----DVNDTWAPVYKAL--YKKEVTKGKTPSPG 180
Qy 262 AFGNIER-----FTY-LKSINAYCSLSLIAAHADGVYGFPRDSSGGAIFPDITKF 313
Db 181 AVONITRGDPAQFVYRAVINAVPEIVEYAVNSTVTKTF-----NTQIADVDFTNF 233

RESULT 9
US-09-410-551B-23
Sequence 23, Application US/09410551B
Patent No. 6503737

GENERAL INFORMATION:
APPLICANT: KOSAN BIOSCIENCES, Inc.
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
FILE REFERENCE: 30062-20026.00
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1509
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
US-09-410-551B-23

Query Match 5.2%; Score 91; DB 4; Length 1509;
Best Local Similarity 19.9%; Pred. No. 3.2;
Matches 37; Conservative 35; Mismatches 70; Indels 44; Gaps 6;

Qy 9 LGNKGQKQTLVLPBG-----VNPNGVASLSQGAVALERKRV----- 49
Db 501 VSSFGVSGTNAHVILAGEVETETPPASPSGDLPLVASRPPALDQRLRLAYLDTTPD 560
Qy 50 --TVESVQPSNRKRYKQVKIQNPTACT-----ANGSCDPSVTRQAVAD 92
Db 561 VDRVAVAQTLARHTFARAVALLGDTVITTPADRPDELVPYSSQGTQHPRMGSG-LAD 619
Qy 93 VTFSTQYSTD--EERAFVETELALLASPLILDAIDOLNPAWTLIA---GGGSGS 145
Db 620 SSVVFAERMAECALAREFVDLFTVLDDPAVVDVNVQPSAWAMVLAIVVQAAGV 679
Qy 146 KPDPVI 151
Db 680 RPDVAVI 685

RESULT 10
US-09-940-316B-23
Sequence 23, Application US/09940316B
Patent No. 6759536
GENERAL INFORMATION:
APPLICANT: KOSAN BIOSCIENCES, Inc.
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520 POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20026.11
CURRENT APPLICATION NUMBER: US/09/940,316B
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/410,551
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748

PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1509
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
OTHER INFORMATION: synthase fragment
US-09-940-316B-23

Query Match 5.2%; Score 91; DB 4; Length 1509;
Best Local Similarity 19.9%; Pred. No. 3.2;
Matches 37; Conservative 35; Mismatches 70; Indels 44; Gaps 6;

QY 9 LGNIGDGGQTLVNLNRG-----VNPTNGVSLSQAGAVPLERKRV----- 49
DB 501 VSFSGVSGTNAHVILTAGPVTETPPASPSGDIPLVVSARSPEALDEQIRLRAYLDTTPD 560
QY 50 --TVSSQSPSRKKNKQVKNPTACT-----ANGSCDPSVTRQAVAD 92
DB 561 VDRVAAGTARHTFAHRAVLGDTVITPPADRPDELVFVSGGCTGHPAWGEO-LAD 619
QY 93 VTFSPQVSTD--ERRAFVTEALALASPLIDAIQINPAVWTLIA---GGSGS 145
DB 620 SSVVFERMAECALAREFDMDLFTVLDPAVVDVVDVQPSAMWMSIAAVWQAGV 679
QY 146 KDPDVT 151
DB 680 RPDVAVI 685

RESULT 11
US-08-455-559-10
Sequence 10, Application US/08455559
Patent No. 5801014

GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR., PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-455-559-10

Query Match 5.1%; Score 90; DB 1; Length 495;
Best Local Similarity 22.0%; Pred. No. 0.71;
Matches 77; Conservative 39; Mismatches 116; Indels 118; Gaps 18;

QY 22 INPRGVNPTNGVSLSQAGAVPA-----LEKRVTSVSDPSR----- 58
DB 116 VTFKQGLP-GKVAS-SKASAPSSFLTKTREPCTPREPKPEFPPPIPTPHEVWLSYRT 173
QY 59 ---NRKRVKQVKNPTACTANGSCD-----PSVTRQAVY-DVTFSPQVSTDEER 106
DB 174 LSDARRKGNSSVKLEAGLANTITSFTIKGDDRGPVARKQVFDI-----SALEKD 226
QY 107 AVFTEALALASPLIDAIQINPAVWT-----LLIAGSGSGSKPVPIDPP 160
DB 227 GLGAEHLRLRKPL-----DVAKPAVSSGSGVADKLSSCSGSGQPAALLDVRSVPGLD 281
QY 161 GTGKYTCPPAIVSLSEVEYEPPTKN-----RPWPIYNAVELQPREF-----DVAL 204
DB 282 GSGWEV--FDIKLFRNF-----KNSAQCLEAWEGRGAVDLRGLGFERTARQVHEKAL 335
QY 205 KOLLGNTKRPDSDSLSTTFRCGCGNGYIDIDAT---YIADQAMROKVIIRGKKRG 261
DB 336 FIVFGTKKRD---LFENEIRARSGOD---DKTYEYLFQRRRRRAPLANRGSKRS 387
QY 262 AFGNTERFYLKINAYCSLS-----DIAAYHADGV 292
DB 388 -----KNLKRCSKRLHYNFKDMGMDWMIAPLEYAHCBEI 426

RESULT 12
US-09-145-060-10
Sequence 10, Application US/09145060
Patent No. 6245896

GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-145-060-10

Query Match 5.1%; Score 90; DB 3; Length 495;
Best Local Similarity 22.0%; Pred. No. 0.71;
Matches 77; Conservative 39; Mismatches 116; Indels 118; Gaps 18;

22 INPGRVPTNGVASLSQAGAVPA-----LEKRVTSVQSPSR----- 58
116 VTPKQGLP-GGKAS-SKAGSAPSSFLKKTREPGTPREPKPEFRPPPTTPHEMYLSYRT 173
59 ---NRKYKQVQKIQNPACTANGSCD-----PSYTRQAYA-DVTFSTQYSTDEER 106
174 LSDADRKGNSSVKEAGLANITTSFIDKGQDRBPAAVKQRVFDI-----SALEKD 226
107 AFVTELAALLASPLLIDAIIDOLNPAWYT-----LLIAGSGSGSKPPVIPPDPIDPP 160
227 GILGAELEILRKRP-----DVAKPAVPSGSRVAQLKLSGCPGQPALLDVRSVPGLD 281
161 GTGKYTCPEAIVSLSEVEVEPTKN-----RPWPIYNAVELQPREF-----DVAL 204
282 GSGMEV--FDIWKLP--KNSAQCLBLEAMERGRAVDRLGCFERTARQVHEKAL 335
205 KDLGNTKWRDMSLSYTFRGCRNGYIDIDAT---YLATDQMRDQKXDIRGKKPG 261
336 FLVFGRTKKRD---LFNEIKARSGOD---DKTVYEYLFQRRKRRAPIANROGKRS 387
262 AFGNIERTIYLSINAYCSLS-----DIAAYHAGCV 292
388 -----KNLKARCSRKALHVNFKDMGMDWIAPLEVEAFHCEGL 426

RESULT 13

PCT-US94-00657-10.
Sequence 10, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUEAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH. D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELEPHONE: 619/445-5100
TELEFAX: 619-445-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-00657-10
Query Match 5.1%; Score 90; DB 5; Length 495;

Best Local Similarity 22.0%; Pred. No. 0.71;
Matches 77; Conservative 39; Mismatches 116; Indels 118; Gaps 18;

22 INPGRVPTNGVASLSQAGAVPA-----LEKRVTSVQSPSR----- 58
116 VTPKQGLP-GGKAS-SKAGSAPSSFLKKTREPGTPREPKPEFRPPPTTPHEMYLSYRT 173
59 ---NRKYKQVQKIQNPACTANGSCD-----PSYTRQAYA-DVTFSTQYSTDEER 106
174 LSDADRKGNSSVKEAGLANITTSFIDKGQDRBPAAVKQRVFDI-----SALEKD 226
107 AFVTELAALLASPLLIDAIIDOLNPAWYT-----LLIAGSGSGSKPPVIPPDPIDPP 160
227 GILGAELEILRKRP-----DVAKPAVPSGSRVAQLKLSGCPGQPALLDVRSVPGLD 281
161 GTGKYTCPEAIVSLSEVEVEPTKN-----RPWPIYNAVELQPREF-----DVAL 204
282 GSGMEV--FDIWKLP--KNSAQCLBLEAMERGRAVDRLGCFERTARQVHEKAL 335
205 KDLGNTKWRDMSLSYTFRGCRNGYIDIDAT---YLATDQMRDQKXDIRGKKPG 261
336 FLVFGRTKKRD---LFNEIKARSGOD---DKTVYEYLFQRRKRRAPIANROGKRS 387
262 AFGNIERTIYLSINAYCSLS-----DIAAYHAGCV 292
388 -----KNLKARCSRKALHVNFKDMGMDWIAPLEVEAFHCEGL 426

RESULT 14

US-09-711-164-312
Sequence 312, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Chisen, Kari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 1569
TYPE: PRT
ORGANISM: Escherichia coli
US-09-711-164-312
Query Match 5.1%; Score 90; DB 4; Length 1569;
Best Local Similarity 20.4%; Pred. No. 4.5;
Matches 81; Conservative 32; Mismatches 143; Indels 142; Gaps 18;

QY 236 LDATYVLTADQMR---DQKXVIRG-KKQGF-----GNIREFYLKSN 276
Db 1323 AGAFEGQLTQMTYTGIDSRNDIPGKITTLGAFMGVSHSHIGFDRGHGSVGSY---SLG 1378
QY 277 AYCSLSDIAATHADQ-----IYFQMDPSGGA 305
Db 1379 GIATWEHSGFTLDGVVLTAFKSNVAG---KMSGGA 1413

RESULT 15
TIC: 09-495

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US-09-485-717-2
Sequence 2, Application US/09485717
Patent No. 6673353
GENERAL INFORMATION:
APPLICANT: Kauffmann, Stefan
APPLICANT: Hess, Jürgen
TITLE OF INVENTION: Tuberculosis Vaccine
FILE REFERENCE: 16862PDS
CURRENT APPLICATION NUMBER: US/09/485,717
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: EP 97114614.7
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PCT/EP98-05109
PRIOR FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 626
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence; recombinant
US-09-485-717-2

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Query Match	5.1%	Score	89.5	DB	4	Length	626
Best Local Similarity	23.5%	Pred	No.1.2				
Matches	31	Conservative	23	Mismatches	43	Indels	35
				Gaps			5

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Db     198 TLISIDIPGMTODNKIIVK--NATKSNNNAVNITLVEWNEKEAQAIVNS---AKIDIYD 252
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QY	104	EERAFV	RT	ELAA	115
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Db	253	DEMAYSE	SQ	LIA	264

Search completed: January 4, 2005, 09:35:42
Job time : 27.8269 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 81.5897 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKETVTLGNIGKDGKQTL.....FTKFDKTKPCIPQAVIVPRA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749	100.0	329	14 US-10-289-454-11	Sequence 11, Appl
2	1749	100.0	329	14 US-10-050-902-217	Sequence 217, App
3	1749	100.0	329	14 US-10-050-898-217	Sequence 217, App
4	1749	100.0	329	14 US-10-346-190-11	Sequence 11, Appl
5	1749	100.0	329	15 US-10-465-811-2	Sequence 11, Appl
6	1749	100.0	329	15 US-10-289-456-11	Sequence 11, Appl
7	1749	100.0	329	15 US-10-622-064-4	Sequence 4, Appl
8	1749	100.0	329	15 US-10-622-124-5	Sequence 5, Appl
9	1749	100.0	329	16 US-10-622-087-5	Sequence 5, Appl
10	1733.5	99.1	328	14 US-10-243-739-11	Sequence 11, Appl
11	1733.5	99.1	328	14 US-10-244-065-11	Sequence 11, Appl
12	978	55.9	329	14 US-10-243-739-16	Sequence 16, Appl
13	978	55.9	329	14 US-10-244-065-16	Sequence 16, Appl

14	978	55.9	329	14 US-10-289-454-16	Sequence 16, Appl
15	978	55.9	329	14 US-10-346-190-16	Sequence 16, Appl
16	978	55.9	329	15 US-10-465-811-7	Sequence 7, Appl
17	978	55.9	329	15 US-10-289-456-16	Sequence 16, Appl
18	978	55.9	329	15 US-10-622-064-28	Sequence 28, Appl
19	978	55.9	329	15 US-10-622-124-10	Sequence 10, Appl
20	978	55.9	329	16 US-10-622-087-10	Sequence 10, Appl
21	978	55.9	330	14 US-10-050-902-254	Sequence 254, App
22	978	55.9	330	14 US-10-050-898-254	Sequence 254, App
23	897.5	51.3	330	14 US-10-243-739-20	Sequence 20, Appl
24	897.5	51.3	330	14 US-10-244-065-20	Sequence 20, Appl
25	897.5	51.3	330	14 US-10-289-454-20	Sequence 16, App
26	897.5	51.3	330	14 US-10-050-902-167	Sequence 167, App
27	897.5	51.3	330	14 US-10-050-898-167	Sequence 167, App
28	897.5	51.3	330	14 US-10-346-190-20	Sequence 20, Appl
29	897.5	51.3	330	15 US-10-465-811-11	Sequence 11, Appl
30	897.5	51.3	330	15 US-10-289-456-20	Sequence 20, Appl
31	897.5	51.3	330	15 US-10-622-064-32	Sequence 32, Appl
32	897.5	51.3	330	15 US-10-622-124-14	Sequence 14, Appl
33	897.5	51.3	330	16 US-10-622-087-14	Sequence 14, Appl
34	663	37.9	132	14 US-10-243-739-10	Sequence 10, Appl
35	663	37.9	132	14 US-10-244-065-10	Sequence 10, Appl
36	663	37.9	132	14 US-10-289-454-10	Sequence 10, Appl
37	663	37.9	132	14 US-10-050-902-159	Sequence 159, App
38	663	37.9	132	14 US-10-050-898-159	Sequence 159, App
39	663	37.9	132	14 US-10-346-190-10	Sequence 10, Appl
40	663	37.9	132	15 US-10-465-811-1	Sequence 1, Appl
41	663	37.9	132	15 US-10-289-456-10	Sequence 10, Appl
42	663	37.9	132	15 US-10-622-064-3	Sequence 3, Appl
43	663	37.9	132	15 US-10-622-124-4	Sequence 4, Appl
44	663	37.9	132	16 US-10-622-087-4	Sequence 4, Appl
45	655	37.4	132	14 US-10-243-739-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-289-454-11
; Sequence 11, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bechmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OR INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT FILING DATE: US/10/289, 454
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396, 636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050, 902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331, 045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta CP
US-10-289-454-11
Query Match 100.0%; Score 1749; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTLGNIGKDGKQTLVLPNGVNPPTNGVASTLSQAGAVPALEKRVTVSVSPSRNR 60
DB 1 MAKETVTLGNIGKDGKQTLVLPNGVNPPTNGVASTLSQAGAVPALEKRVTVSVSPSRNR 60

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DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTELAALLASP 120
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DB 121 L1IDAIDQNPAYWTLIIAGGSGSKPDVPIPPPIIDPPPGTKYTCPPAIIISLEEVYEP 180
QY 181 PTKNRPMPIYNNAVELQPREFDVALKDLGNTKMRDMSRLSTYTFRGCRNGYIIDDATY 240
DB 181 PTKNRPMPIYNNAVELQPREFDVALKDLGNTKMRDMSRLSTYTFRGCRNGYIIDDATY 240
QY 241 LATDQMRQKDYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 300
DB 241 LATDQMRQKDYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 300
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DB 301 SSGGAIIPFDFTKDKTCPIQAVIYVPR 329
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RESULT 2

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US-10-050-902-217
; Sequence 217, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisoc, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050, 902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262, 379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288, 549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326, 998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331, 045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 217
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-050-902-217
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Query Match 100.0%; Score 1749; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 3, 8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTELAALLASP 120
QY 121 L1IDAIDQNPAYWTLIIAGGSGSKPDVPIPPPIIDPPPGTKYTCPPAIIISLEEVYEP 180
DB 121 L1IDAIDQNPAYWTLIIAGGSGSKPDVPIPPPIIDPPPGTKYTCPPAIIISLEEVYEP 180
QY 181 PTKNRPMPIYNNAVELQPREFDVALKDLGNTKMRDMSRLSTYTFRGCRNGYIIDDATY 240
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QY 301 SSGGAIIPFDFTKDKTCPIQAVIYVPR 329
DB 301 SSGGAIIPFDFTKDKTCPIQAVIYVPR 329
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RESULT 3

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US-10-050-898-217
; Sequence 217, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisoc, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staudenbier, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050, 898
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262, 379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288, 549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326, 998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331, 045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 217
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-050-898-217
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Query Match 100.0%; Score 1749; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 3, 8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRNR 60
QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTELAALLASP 120
DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTELAALLASP 120
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DB 121 L1IDAIDQNPAYWTLIIAGGSGSKPDVPIPPPIIDPPPGTKYTCPPAIIISLEEVYEP 180
QY 181 PTKNRPMPIYNNAVELQPREFDVALKDLGNTKMRDMSRLSTYTFRGCRNGYIIDDATY 240
DB 181 PTKNRPMPIYNNAVELQPREFDVALKDLGNTKMRDMSRLSTYTFRGCRNGYIIDDATY 240
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Db 301 SSGGAIPEDFTKFDKTCPIQAVIVPRA 329

RESULT 7

US-10-622-064-4
; Sequence 4, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Qbeta
US-10-622-064-4

Query Match 100.0%; Score 1749; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPITNGVASLSQAGAVPALERKVTVSQPSRNR 60
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Db 61 KNYKVQVXIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVFTLALLASP 120
QY 121 LIIDAIDQNPAYWTLIIAGGSGSKDPVLPDPIDPPGTGKTCPPAIVMSLEVEYEP 180
Db 121 LIIDAIDQNPAYWTLIIAGGSGSKDPVLPDPIDPPGTGKTCPPAIVMSLEVEYEP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTFRGCRNGYIDL DATY 240
Db 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTFRGCRNGYIDL DATY 240
QY 241 LATDQAMRDQKDIRGKKRGAFGNIERFIYKXSINAYCSLSDIAAYHADGVI VGFWRDP 300
Db 241 LATDQAMRDQKDIRGKKRGAFGNIERFIYKXSINAYCSLSDIAAYHADGVI VGFWRDP 300
QY 301 SSGGAIPEDFTKFDKTCPIQAVIVPRA 329
Db 301 SSGGAIPEDFTKFDKTCPIQAVIVPRA 329

RESULT 8

US-10-622-124-5
; Sequence 5, Application US/10622124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulturja, Alma
; TITLE OF INVENTION: Ghrelin-Carrier Conjugates
; FILE REFERENCE: 1700.0340001
; CURRENT APPLICATION NUMBER: US/10/622,124
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,638
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-622-124-5

Query Match 100.0%; Score 1749; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPITNGVASLSQAGAVPALERKVTVSQPSRNR 60
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Db 61 KNYKVQVXIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVFTLALLASP 120
QY 121 LIIDAIDQNPAYWTLIIAGGSGSKDPVLPDPIDPPGTGKTCPPAIVMSLEVEYEP 180
Db 121 LIIDAIDQNPAYWTLIIAGGSGSKDPVLPDPIDPPGTGKTCPPAIVMSLEVEYEP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTFRGCRNGYIDL DATY 240
Db 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTFRGCRNGYIDL DATY 240
QY 241 LATDQAMRDQKDIRGKKRGAFGNIERFIYKXSINAYCSLSDIAAYHADGVI VGFWRDP 300
Db 241 LATDQAMRDQKDIRGKKRGAFGNIERFIYKXSINAYCSLSDIAAYHADGVI VGFWRDP 300
QY 301 SSGGAIPEDFTKFDKTCPIQAVIVPRA 329
Db 301 SSGGAIPEDFTKFDKTCPIQAVIVPRA 329

RESULT 9

US-10-622-087-5
; Sequence 5, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tisbec, Alain
; APPLICANT: Ottmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Mathias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
; FILE REFERENCE: 1700.0350002
; CURRENT APPLICATION NUMBER: US/10/622,087
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,639
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/470,432
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 329

TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-087-5

Query Match 100.0%; Score 1749; DB 16; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSOPSRR 60
DB 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSOPSRR 60
QY 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTEIAALIASP 120
DB 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTEIAALIASP 120
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DB 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVIPPDPIDPPGKTKCPAIAISLEEVYP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTFRGCRGNGYIDLATY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTFRGCRGNGYIDLATY 240
QY 241 LATDQAMDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYVGFWRDP 300
DB 241 LATDQAMDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYVGFWRDP 300
QY 301 SSGGAIIPDFTFKDKTKCPIQAVIYVPPRA 329
DB 301 SSGGAIIPDFTFKDKTKCPIQAVIYVPPRA 329

RESULT 10
US-10-243-739-11

Sequence 11, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243, 739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318, 967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 328
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-11

Query Match 99.1%; Score 1733.5; DB 14; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.2e-159;
Matches 328; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSOPSRR 60
DB 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSOPSRR 60
QY 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTEIAALIASP 120
DB 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTEIAALIASP 120
QY 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVIPPDPIDPPGKTKCPAIAISLEEVYP 180
DB 121 LIIIDAIDQNPAYW-TLIIAGGSGSKPDVIPPDPIDPPGKTKCPAIAISLEEVYP 179
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTFRGCRGNGYIDLATY 240

DB 180 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTFRGCRGNGYIDLATY 239
QY 241 LATDQAMDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYVGFWRDP 300
DB 240 LATDQAMDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYVGFWRDP 299
QY 301 SSGGAIIPDFTFKDKTKCPIQAVIYVPPRA 329
DB 300 SSGGAIIPDFTFKDKTKCPIQAVIYVPPRA 328

RESULT 11
US-10-244-065-11

Sequence 11, Application US/10244065
Publication No. US2003009968A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazio
APPLICANT: Maurel, Patrick
APPLICANT: Tisoc, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244, 065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374, 145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318, 994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 328
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-11

Query Match 99.1%; Score 1733.5; DB 14; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.2e-159;
Matches 328; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSOPSRR 60
DB 1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSOPSRR 60
QY 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTEIAALIASP 120
DB 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEBERAFVTEIAALIASP 120
QY 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVIPPDPIDPPGKTKCPAIAISLEEVYP 180
DB 121 LIIIDAIDQNPAYW-TLIIAGGSGSKPDVIPPDPIDPPGKTKCPAIAISLEEVYP 179
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTFRGCRGNGYIDLATY 240
DB 180 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTFRGCRGNGYIDLATY 239
QY 241 LATDQAMDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYVGFWRDP 300
DB 240 LATDQAMDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYVGFWRDP 299
QY 301 SSGGAIIPDFTFKDKTKCPIQAVIYVPPRA 329
DB 300 SSGGAIIPDFTFKDKTKCPIQAVIYVPPRA 328

RESULT 12
US-10-243-739-16
Sequence 16, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage SP
US-10-243-739-16

Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3,4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 2 AKLEVTTLGNIGKDGKQTLVNLPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 61
DB 1 AKLNOVTLSTKIGKNDQTLTLPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 60
QY 62 NYKVOVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTEIAALLASPL 121
DB 61 NEKVOIKIQNPACTRD-ACDPSVTRSAFADVTLSTQYSTDEBERALIRTEIAALLADPL 119
QY 122 LIDAIDQNPAYW-TLLIAGGSGSKPD---PVLPDPIDPPPGTKYTCFPAIWSLEB 176
DB 120 IYDAIDNINPAYWALLVASSGGSDNPDPVPVVD--VKPPDGTGRYKCFACRYLGS 177
QY 177 VPEPTKRPMPVINAVALQPREPDVALKDLGNTKMDPSRLS---YTFPGCGRGNGY 233
DB 178 IYEVGKESGP-DIYRGDEVSTFEDYALDEPLGNTNMRMDQRLSDYDIANRRRCRGNGY 236
QY 234 IDLDATYATDQMRDQKDIYREGKKPGAFGNIERYFYLSI--NAYCSLSIDIAAYHADG 291
DB 237 IDLDATAMQSDDFVLSGRYGVKVFPGAFGSIK---YLLNIGDAMLDLSEVTAYRSYG 293
QY 292 VIVGFWRPDSSGGAIPFDTKFKDKTCPIQAVIYVP 327
DB 294 MVIGFWTD-SKSPQLPDTQFNSANCPVQTVIILP 328

RESULT 13
US-10-244-065-16
Sequence 16, Application US/10244065
Publication No. US20030093668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tisbet, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerd
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofs, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145

PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage SP
US-10-244-065-16

Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3,4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 2 AKLEVTTLGNIGKDGKQTLVNLPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 61
DB 1 AKLNOVTLSTKIGKNDQTLTLPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 60
QY 62 NYKVOVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTEIAALLASPL 121
DB 61 NEKVOIKIQNPACTRD-ACDPSVTRSAFADVTLSTQYSTDEBERALIRTEIAALLADPL 119
QY 122 LIDAIDQNPAYW-TLLIAGGSGSKPD---PVLPDPIDPPPGTKYTCFPAIWSLEB 176
DB 120 IYDAIDNINPAYWALLVASSGGSDNPDPVPVVD--VKPPDGTGRYKCFACRYLGS 177
QY 177 VPEPTKRPMPVINAVALQPREPDVALKDLGNTKMDPSRLS---YTFPGCGRGNGY 233
DB 178 IYEVGKESGP-DIYRGDEVSTFEDYALDEPLGNTNMRMDQRLSDYDIANRRRCRGNGY 236
QY 234 IDLDATYATDQMRDQKDIYREGKKPGAFGNIERYFYLSI--NAYCSLSIDIAAYHADG 291
DB 237 IDLDATAMQSDDFVLSGRYGVKVFPGAFGSIK---YLLNIGDAMLDLSEVTAYRSYG 293
QY 292 VIVGFWRPDSSGGAIPFDTKFKDKTCPIQAVIYVP 327
DB 294 MVIGFWTD-SKSPQLPDTQFNSANCPVQTVIILP 328

RESULT 14
US-10-289-454-16
Sequence 16, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sondergeger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage SP CP
US-10-289-454-16

Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3,4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 2 AKLEVTTLGNIGKDGKQTLVNLPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 61

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Db 1 AKLNGVTLSKIGKNDQTLTLTPRGVNPNGVASISSEAGAVPALERKRVTVSAQPSRNK 60
Qy 62 NYKVQVKIONPACTANGSCDPSVTRQAYADYTFSTQSTDEBRAFAVTEIAALLASPL 121
Db 61 NFKVQIKONPACTCRD-ACDPSVTRSAFADYTLSTSTDEBRALITETIAALLADPL 119
Qy 122 LIDAIQOLNPAYW-TLLIAGGSGSKPD---PVIIDPPIIDPPGTYKTCFPAIWSLEB 176
Db 120 IYDAIDNLNPAYWALLVASSGGGNPSPDPVVPVDP--VKPPDGTGRYKCPACVRLGS 177
Qy 177 VYEPPTKRPMPPIYNAVELQPREFDVALKOLLGNTKRWDSRLS---YTTTRGCRNGY 233
Db 178 IYEVGKEGSP-DIYERGDEVSYTFDYALDFLGNTNWRNWDQRLSDYDIANRRRCRNGY 236
Qy 234 IDLDATYLATQAMBDQKYDIREGKKPGAFGNIERFIYLSI--NAYCSLSDIAAYHADG 291
Db 237 IDLDATAMQSDPFVLSGRYGRKVKFPGAFSGIK--YLLNTIQGAMWLDLSEVTAYRSYG 293
Qy 292 VIVGFWRDPSSGGAIPDFTFKFDKTKCPIQAVIYVP 327
Db 294 NVIGFWTD-SKSPQLPTDFTQFNNSANCPVQTVIIIP 328
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RESULT 15

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US-10-346-190-16
; Sequence 16, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurel, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 329
; TYPE: prt
; ORGANISM: RNA-phage SP A1 protein
US-10-346-190-16
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Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred No. 3,4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;
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Qy 2 AKLETVTLGNIKGDKQTLVLNPRGVNPTNGVASISQAGAVPALERKRVTVSVQPSRNK 61
Db 1 AKLNGVTLSKIGKNDQTLTLTPRGVNPNGVASISSEAGAVPALERKRVTVSAQPSRNK 60
Qy 62 NYKVQVKIONPACTANGSCDPSVTRQAYADYTFSTQSTDEBRAFAVTEIAALLASPL 121.
Db 61 NFKVQIKONPACTCRD-ACDPSVTRSAFADYTLSTSTDEBRALITETIAALLADPL 119
Qy 122 LIDAIQOLNPAYW-TLLIAGGSGSKPD---PVIIDPPIIDPPGTYKTCFPAIWSLEB 176
Db 120 IYDAIDNLNPAYWALLVASSGGGNPSPDPVVPVDP--VKPPDGTGRYKCPACVRLGS 177
Qy 177 VYEPPTKRPMPPIYNAVELQPREFDVALKOLLGNTKRWDSRLS---YTTTRGCRNGY 233
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Db 178 IYEVGKEGSP-DIYERGDEVSYTFDYALDFLGNTNWRNWDQRLSDYDIANRRRCRNGY 236
Qy 234 IDLDATYLATQAMBDQKYDIREGKKPGAFGNIERFIYLSI--NAYCSLSDIAAYHADG 291
Db 237 IDLDATAMQSDPFVLSGRYGRKVKFPGAFSGIK--YLLNTIQGAMWLDLSEVTAYRSYG 293
Qy 292 VIVGFWRDPSSGGAIPDFTFKFDKTKCPIQAVIYVP 327
Db 294 NVIGFWTD-SKSPQLPTDFTQFNNSANCPVQTVIIIP 328
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Search completed: January 4, 2005, 09:41:21
Job time : 82.5897 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 19.6637 Seconds

(without alignment)
1609.836 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKETVTLGNIGKDGKQTL.....FTKPKTKCPIQAVIVPRA 329Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summariesDatabase :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	983	56.2	331	2	readthrough protei
2	663	37.9	132	1	coat protein - pha
3	117	6.7	131	1	coat protein - pha
4	113.5	6.5	409	2	conserved hypochel
5	106	6.1	973	2	probable secreted
6	95.5	5.5	1326	2	probable ATP-depen
7	95	5.4	915	2	cellulase (EC 3.2.
8	94.5	5.4	530	2	seeligerolysin -
9	94	5.4	501	2	growth/differentia
10	93.5	5.3	540	2	hypothetical prote
11	93	5.3	439	2	glutamine syntheta
12	93	5.3	974	1	optic lobe develop
13	92.5	5.3	983	2	polymorphic membra
14	92	5.3	385	2	hypothetical prote
15	91.5	5.2	1461	2	hypothetical prote
16	91.5	5.2	1461	2	hypothetical prote
17	91	5.2	609	2	hypothetical prote
18	90.5	5.2	280	2	transcription fact
19	90.5	5.2	836	2	hypothetical prote
20	90.5	5.2	836	2	hypothetical prote
21	90.5	5.2	1302	2	hypothetical prote
22	90.5	5.2	1785	2	hypothetical prote
23	90	5.1	495	2	major merizole su
24	90	5.1	1569	2	bone morphogenetic
25	90	5.1	1612	2	hypothetical prote
26	89.5	5.1	1612	2	ductil protein - mo
27	89.5	5.1	529	2	probable tellurium
28	89.5	5.1	529	2	listeriolysin prec
29	89.5	5.1	529	2	listeriolysin O pr
					listeriolysin O pr

30	89	5.1	949	2	T08658	hypothetical prote
31	89	5.1	1039	2	S02711	cellulase (EC 3.2.
32	88.5	5.1	830	2	S57537	MKRI protein - yea
33	88.5	5.1	1307	2	T35944	probable beta-gala
34	88	5.0	928	2	C81265	probable lipoprote
35	88	5.0	978	2	D81411	probable lipoprote
36	87	5.0	346	2	B60340	transposase - Myco
37	87	5.0	346	2	H70567	transposase - Myco
38	86.5	4.9	476	2	B44997	merozoitte surface
39	86.5	4.9	593	2	F64523	hypothetical prote
40	86	4.9	130	1	A46324	coat protein - pha
41	86	4.9	408	2	S54813	probable chain len
42	86	4.9	793	2	T41703	dipeptidyl aminope
43	86	4.9	850	2	S56015	gastric mucin MUC5
44	86	4.9	933	2	S41539	fibrinogen-binding
45	85.5	4.9	312	2	A56911	TRAD protein - hu

ALIGNMENTS

RESULT 1

readthrough protein - phage SP

C/Species: phage SP
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004C/Accession: S01964
R/Inokuchi, Y.; Jacobson, A.B.; Hirose, T.; Inayama, S.; Hiraehima, A.Nucleic Acids Res. 16, 6205-6221, 1988
A/Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP.A/Reference number: S01963; MUID:88289362; PMID:339390
A/Accession: S01964A/Status: preliminary
A/Molecule type: genomic RNAA/Residues: 1-331 <INO>
A/Cross-references: UNIPROT:P09677; EMBL:X07489

A/Note: the authors translated the readthrough stopcodon TGA for residue 133 as Trp

C/Superfamily: phage GA coat protein

Query Match	Score	983	DB 2	Length	331
Best Local Similarity	56.2%				
Matches	197				
Conservative	45				
Mismatches	77				
Indels	18				
Gaps	9				
QY	1	MAKETVTLGNIGKDGKQTLVLPNGVNPNGVNLGASLQAGVPALEKRVTVSVQPSNR	60		
DB	1	MAKNQVTLGKDGKQDQTLITPRGVNPTNGVNLSEGAVALPKVTVSVQPSNR	60		
QY	61	KNYKVQVKIQNPTACTANGSCDPSVTRQAVADVTFSTQYSTDERRAFVRIELALLASP	120		
DB	61	KNFKVQIKIQNPTACTRD-ACDPSVTRSAFADVTLFSTYSDERRALRIELALLADP	119		
QY	121	LIIIDAIDQNPVYM-TLIIAGGSGSKPD---PYIPDPIDPPGCTGKVTCPFAIWSLE	175		
DB	120	LIVDAIDNPVYMALIVASSGGDNPSPDPVAVPD-VKPPGCTGKVKPFCYRIG	177		
QY	176	EYVEPPTKRPMPVYNAYELQPREPVALKDILGNTKRMQMDPSRLS---YTFRCGRGNG	232		
DB	178	STYVEGKSGSP-DIERGDVSVTFDVALIEDPLGNTMRNMQRLSDVIDIARRRCRNG	236		
QY	233	YIDDATYIADQANDQKVDIREGKKGAFNGIERFIYLSI--NAYCSLSDIAYHAD	290		
DB	237	YIDLDATAMQSDDFVLSRGYGVKVPFGAFSGISK---YLIINIQGDAMLDISEVAYRSY	293		
QY	291	GIVVGFWRDPSGGAIPDFTEKEDTKPCIQAVIVP	327		
DB	294	GVVIGFWTD-SKSPQLPTDFQFNSANCPCVQTVIITP	329		

RESULT 2

coat protein - phage Q-beta

C/Species: phage Q-beta
C/Date: 29-Jul-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004

C/Accession: A92240; A92221; A92088; A04224
 R/Becarrm9, C.; Saeary, P.A.; Billeter, M.A.
 J. Biol. Chem. 253, 8390-8399, 1978
 A/Title: Determination of the first half of the coat protein cistron of bacteriophage Qb
 A/Reference number: A92240; MID:79048469; PMID:361741
 A/Accession: A92240
 A/Molecule type: mRNA
 A/Residues: 1-80 <ESC>
 A/Cross-references: UNIPROT:P03615
 R/Stoll, E.; Wilson, K.J.; Reiser, J.; Weissmann, C.
 J. Biol. Chem. 252, 990-993, 1977
 A/Title: Reversed amino acid sequence of Qbeta coat protein between positions 1 and 60.
 A/Reference number: A92221; MID:77118576; PMID:838709
 A/Accession: A92221
 A/Molecule type: protein
 A/Residues: 1-60 <STO>
 R/Malta, T.; Konigsberg, W.
 J. Biol. Chem. 246, 5003-5024, 1971
 A/Title: The amino acid sequence of the Qbeta coat protein.
 A/Reference number: A92088; MID:71288580; PMID:5570434
 A/Accession: A92088
 A/Molecule type: protein
 A/Residues: 1-21; D, 23-55, 57-132 <MAI>
 C/Superfamily: phage GA coat protein

Query Match 37.9%; Score 663; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLEVTTLNIGKDGKQTLVLPNGVNPFTNGVASLSQAGVPALEKRVTVSVSQPSRNK 61
 DB 1 AKLEVTTLNIGKDGKQTLVLPNGVNPFTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 QY 62 NYVQVXKIONPCTANGSCDPSVTROAVYDVFSTQYSTDERAFVRETLAALLASPL 121
 DB 61 NYVQVXKIONPCTANGSCDPSVTROAVYDVFSTQYSTDERAFVRETLAALLASPL 120
 QY 122 LIDAIQDQNPAY 133
 DB 121 LIDAIQDQNPAY 132

RESULT 3
 VCBPPI
 coat protein - phage PRRI
 C/Species: phage PRRI
 C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
 R/Accession: A04225
 R/Dhaese, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
 Eur. J. Biochem. 94, 375-386, 1979
 A/Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage Qb
 A/Reference number: A04225; MID:7918387; PMID:107028
 A/Accession: A04225
 A/Molecule type: protein
 A/Residues: 1-131 <DNA>
 A/Cross-references: UNIPROT:P03616
 C/Superfamily: phage GA coat protein

Query Match 6.7%; Score 117; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.011;

Matches 42; Conservative 15; Mismatches 57; Indels 16; Gaps 5;

QY 18 QTLVLPNGVNPFT-----NGVASLSQAGVPALEKRVTVSVSQPSRNKRVTVSV 67
 DB 4 QNLVLDREKATPDHDFVPPDIRDNGVEVSTGCVPIGESRFTISLRKSNGR--YKSTL 61
 QY 68 KIONPT--ACTANGSCDPSVTROAVYDVFSTQYSTDER--AFVRETLAALLASPLLI- 123
 DB 62 KLVVPPVQSGTVNGIVTPVVVTRTSYTVDEPDYDARSITKERNRNFVGMIALAKADMLVH 121
 QY 124 DAIDQDNPAY 133
 DB 122 DTIVNLQGVY 131

RESULT 4

D90268
 conserved hypothetical protein [imported] - Sulfolobus solfataricus
 C/Species: Sulfolobus solfataricus
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 A/Accession: D90268
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y
 Jung, I.; Jeffries, A.C.; Konzer, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 arett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to Genbank, April 2001
 A/Description: Sulfolobus solfataricus complete genome.
 A/Reference number: A99139
 A/Accession: D90268
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-409 <KUR>
 A/Cross-references: UNIPROT:Q97Y27; GB:AE006641; NID:g13814341; PIDN:AAK1403.1; GSPDB:G
 C/genetics:
 A/Gene: SS01152

Query Match 6.5%; Score 113.5; DB 2; Length 409;
 Best Local Similarity 23.0%; Pred. No. 0.096;

Matches 62; Conservative 36; Mismatches 99; Indels 73; Gaps 13;

QY 89 AYADVTFSPTQYSTDERAFVRETLAAL-----LASPL-----LIDAIQDQNP 131
 DB 160 AFSSTSFSSQYKDSIKRA---NELASITGKKEITRGKVDILSLPVMGNLMESVARNAS 216
 QY 132 AY-----WTLIAGGSGSKDPVITPDPIDP-----PQT-----GKTCPF 169
 DB 217 GVAIMGSMMLKPGKAGSDKFTLDTPEKDRPNMGPEDECTFTYKKAIIENGVEFTPL 276
 QY 170 AIMSLEBYE--PPTKNRPIYNAVELOPREGVALIKDGL-----NTKMDWSRLSX 222
 DB 277 LNNELSNVFKLPSTGNAGVITYPTANNLEVEGSDTFSLSGNVVFYINVM-----Y 328
 QY 223 TFRGCGNGYIDLATYLATDQAMRDQYDIREKKPGAFGNIRFIYLSINAYCSLS 282
 DB 329 TRFQ-----NVAEGPSTVA-----RDATVVRNQNPGVIGRVLADLKLKI-----LK 373
 QY 283 DIAAHADGVITGFMRDPSGGAIPDPFTK 312
 DB 374 NIVELSRERYSVWMDAPWQ--GVYPAVLAK 402

RESULT 5

T35238
 probable secreted cellulase - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 R/Accession: T35238
 R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, September 1998
 A/Reference number: Z21572
 A/Accession: T35238
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-973 <SEE>
 A/Cross-references: UNIPROT:O86728; EMBL:AL031515; PIDN:CAA20643.1; GSPDB:GN00070; SC0EDB
 A/Experimental source: strain A3(2)
 C/genetics:
 A/Gene: SC0EDB:SC5C7.31c

Query Match 6.1%; Score 106; DB 2; Length 973;
 Best Local Similarity 23.4%; Pred. No. 1.3;

Matches 47; Conservative 24; Mismatches 86; Indels 44; Gaps 10;

QY 138 IAGGSGSKDPVITPDPIDPPTGKGYCPAIVMSLEVEBPPTKN-----RMPPIYNA 192
 DB 717 IAGGATSNAGR-YATPAGTPTFGMY-----YDEKPYVHPDPSNGMFGQANSMERV 769

QY 193 VELQREPVVAKDLGNTKRDMSRLSYTTPRCGRNGYIDLDATYATLTDQAMRDQY 252
Db 770 AEYQOOSGAGAKAVL--DKWVDM--ALSEIT-----VNPDETFRPISTLTQWGGP 816
QY 253 DUREGKKPGAFG--NIERFIYLSKINAYCSLSIDIAVHAD-----GVIVGFWR 298
Db 817 DTWNASPEANDDHVEVADYTNVGVAAVAKTLTYTADRSGDTRAASTAKALLDGMFE 876
QY 299 D--PSSGGAIP--FDPTKED 314
Db 877 NNQDALGIAPVETRADYNNRFD 897

RESULT 6
H33232
Probable ATP-dependent helicase PA3297 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #ext_change 09-Jul-2004
C/Accession: H83232
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Muzoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: AB2950; MUID:20437357; PMID:10984043
A/Accession: H83232
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1326 <STO>
A/Cross-references: UNIPROT:Q9HYI6; GB:AE004752; GB:AE004091; NID:G9949424; PIDD:AA60668
A/Experimental source: strain PA01
A/Gene: PA3297
Query Match
Best Local Similarity 5.4%; Score 95.5; DB 2; Length 1326;
Matches 92; Conservative 48; Mismatches 124; Indels 105; Gaps 25;
QY 17 KOTLVNPRG---VNPNGVASISQAGAVPALEKEKTVSVSQPSHNRKRYKVQ-VKION 71
Db 338 EQQKIFQPRPKRKIVLSTN-VAETSL--TVPGIRYIDSGTARISRYRAKQRLPIEA 394
QY 72 PACTAN-----GSCDPSVTRQAVDVTPFTQYSTDERAFVTELAALASPIL--- 122
Db 395 VQASANQKRGKRGVPGICVRLYSEBDFNAPATDPE--ILRTNLAIVILQMLHLRL 452
QY 123 --IDAIDQANPA-----YMTLL--IAGGSGSKRDPV---IPDPPIPRP----- 161
Db 453 GDIENAPFIEPPDGKAIKDGFTLLQELSAVNRGQLTPGROQLARLPIDPRIGRMILLEAA 512
QY 162 -TGKATCPFAIWSLEVEYPTKRPMPYNAVELQ--PREFVALKDLR--GNTKWRMD 217
Db 513 QQG-----SLEEVL-----TYASALSVDPREPRPERQOADDQMAQMKDPD 554
QY 218 SRLS--YTFRG-----CRGN--GYIDL---DA---TYLATDQAM-- 247
Db 555 SDFALINIMRGREBQROALGSNALRSWCKNFPLNTLRLEWMDARQLTLICRELKLPF 614
QY 248 -RDQKDIIEGK-KPAFNGIERFI---YLSKINAYCS--LSDIAYHADVIVG---- 295
Db 615 GPPAKAEAKPEKKGASADNREVEPIDYAAVHKAITLGLLSQIQKAEGBGYLAGOR 674
QY 296 -FWRDPSSG 303
Db 675 RFWIHPSG 683

RESULT 7
A43802
Cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellulohydrolase (EC 3.2.1.91) - Caldocellum
N/Alternate names: endo-1,4-beta-glucanase
C/Species: Caldocellum saccharolyticum
C/Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #ext_change 15-Mar-2004

C/Accession: A43802
R/Saul, D.V.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L.
Appl. Environ. Microbiol. 56, 3117-3124, 1990
A/Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile "C
A/Reference number: A43802; MUID:91136262; PMID:2126700
A/Accession: A43802
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A/Molecule type: DNA
A/Residues: 1-915 <SAU>
A/Cross-references: EMBL:X13602
C/Function:
A/Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cel
A/Pathway: cellulose degradation
A/Keywords: glycosidase; hydrolase, polysaccharide degradation
F/20-320/Domain: Streptomyces endo-1,4-beta-xylanase [A homology <XY>

Query Match
Best Local Similarity 5.4%; Score 95; DB 2; Length 915;
Matches 54; Conservative 38; Mismatches 108; Indels 44; Gaps 12;
QY 90 YADVTFSTQYSTDERAFVTELAALASPILIDAIDLPAYVTLIAGGSGSKPDP 149
Db 271 YKNVKSVTFWGLKQDYSWLRG-FYKNDWPLLFEDYSAKPAAVMAVIAAGVTTSSPTP 329
QY 150 -----VLPDPIDPPETGKTYTCEPAIWSLEVEYPTKRPMPYNAVELQREFPV 202
Db 330 TPTPTVTVPTPTPTPTPG-GQIK--VYANKETNSTNTNTRPW--LRVNSGSSSIDL 383
QY 203 ALKDLGNTKRDMSRLSYTTPRCGRNGYIDLDATYATLTDQAMRDQYDUREGKKPG 262
Db 384 SRVTL--RYMTTVDERQASVSDWAQIGASVTFKFKYLSVSGADYILEIGKSGH 440
QY 263 -----FGNIE-RF-----YIKSINAYCSLSIDIAVHADGYIVGFWR 298
Db 441 GOLQPKGTGELQIRFNKSDMSNNGNDMSWLSQSTVSGEMEKVAY-IDGLV--WQ 497
QY 299 DPGS 302
Db 498 EPST 501

RESULT 8
S22340
seeligeriolysin - Listeria seeligeri
C/Species: Listeria seeligeri
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #ext_change 09-Jul-2004
C/Accession: S22340
R/Haas, A.; Dumbeky, M.; Kreft, U.
Biochim. Biophys. Acta 1130, 81-84, 1992
A/Title: Listeriolysin genes: complete sequence of llo from Listeria ivanovii and of lso
A/Reference number: S22340; MUID:92182018; PMID:1543752
A/Accession: S22340
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-530 <HAA>
A/Cross-references: UNIPROT:P31830; EMBL:X60462; NID:G44144; PIDD:CAA42996.1; PID:G44145
A/Note: the authors translated the codon GCC for residue 287 as Pro
C/superfamily: dipeptide transport protein

Query Match
Best Local Similarity 5.4%; Score 94.5; DB 2; Length 530;
Matches 34; Conservative 23; Mismatches 40; Indels 35; Gaps 7;
QY 14 KDGKQTLV--NPRGVNPT-----NGVASISQAGA-----VPALEKRY 49
Db 94 KDGSEIVVEKKKKGINNADISVINAISLTYPAALYKANRELVENPNVLPVKRDSL 153
QY 50 TVSVSQPSHNRKRYKQVQKIONPTACTANGSCDPSVTR-----QAYADVTFSTQYSTP 103
Db 154 TISVLDLPGMTKDKDKIFVR--NPTKSNVNAVNTLVERNDKYSKAYPRINAKI-DYS-- 208
QY 104 EEPAPVTELA 115

DB 209 DENAYESOLIA 220

RESULT 9

JC2347 growth/differentiation factor 5 - human

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: JC2347

R/Author: G. J. Neidhardt, H. J. Jacobowsky, B. J. Pohl, J.

Biochem. Biophys. Res. Commun. 204, 646-652, 1994

A/Title: Cloning and expression of recombinant human growth/differentiation factor 5.

A/Reference number: JC2347; PMID:95071375; PMID:7980526

A/Accession: JC2347

A/Molecule type: DNA

A/Residues: 1-501 <HOE>

A/Cross-references: UNIPROT:P43026; GB:X80915; NID:g671524; PIDN:CAA56874.1; PID:g671525

C/Genetics:

A/Status: GDB:BMP9

A/Cross-references: GDB:433948

A/Introns: 211/1

C/Superfamily: Inhibin

C/Keywords: glycoprotein

F/89/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 5.4%; Score 94; DB 2; Length 501;

Best Local Similarity 21.7%; Pred. No. 5.5; Matches 77; Conservative 35; Mismatches 115; Indels 128; Gaps 18;

22 LNRRGVNPTNGVASLSQAGAVP-----ALEKRVTVSVQSPR----- 58

122 VPEKGLP--GKAPKAGSVPSFLKKAREGPPEPRPPPTTPEHEYMLSLYR 179

59 -----NRKNVQVQKIQNPACTANGSCD-----PSYTRQAAV-DYTESFTQYDDEER 106

180 LSDADKKGNSVYLEGLANTTSPDKQDDRPVVRKQYVFDI-----SALBKD 232

107 AFVRETEALALAPLIDALDQNPAYWTLIAGG-----SGSKPPVPIPDPP 155

233 GLGALRLIRKKP-----SDTAKPA-----APGGRAAQLKUSCPSGQPSLIDVS 282

156 IDPPGTGKTCPPAIWSLEVEYEPPTKN-----RPMPYNAVELQPREFDVALKD- 206

283 VPELDSDSGWEV--FDIMKLFRRN-----KNSAQLCLELAWERGRAVDLRLGFDRAARQV 336

207 -----LIGNTKWRWDSRLSYTTRGCGNGYIDLDAT--YLAITDQMRDQKTDIRE 256

337 HEKALFLVGRRTKKD-----LFNEIKANSQD-----DKTVRYLFSQRRKRAPIATRO 388

257 GKRGAFGNIERPIYLSKINAYCSLS-----DIAAYHADGV 292

389 GKRRS-----KNLKARCSRKALHVPKMGMDWITIALEAEAHCEGL 432

RESULT 10

T00646 hypothetical protein F316.9 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C/Accession: T00646

R/Author: N.A.; Palm, C.U.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo, R.; Federspiel, N.A.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.

submitted to the EMBL Data Library, February 1998

A/Reference number: Z14197

A/Accession: T00646

A/Status: translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-540 <FED>

A/Cross-references: UNIPROT:O48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g2

C/Genetics:

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-974 <PFL>

A/Cross-references: UNIPROT:Q24432; GB:M81796; NID:g158018; PIDN:AAA28736.1; PID:g158019

A/Note: sequence extracted from NCBI backbone (NCBI:82056)

R/Author: B.; Balles, U.; Pflugfelder, G.O.

Mol. Gen. Genet. 238, 325-332, 1993

A/Title: Transcript identification in the optomotor-blind locus of Drosophila melanogaster

A/Reference number: S34827; PMID:93261414; PMID:8492800

A/Introns: 14/3; 281/3; 428/3; 448/2; 483/3; 502/3

C/Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binc

Query Match 5.3%; Score 93.5; DB 2; Length 540;

Best Local Similarity 27.8%; Pred. No. 6.7; Matches 32; Conservative 14; Mismatches 54; Indels 15; Gaps 3;

12 IGDGKQTLVLPNG--VNPTNGVASLSQAGAVPALKERVTVSVQSPRKN-KYQV 67

255 VKKEKKPNLKKNDGNVRINPTGRSLKPVQGVGKPEPTNTVTSRKTPPEKEMNMKATK 314

68 KQNPACTRANGSCDPSVTRQAVDYTESFTQYSDIEEAAPRTIELAALAPFL 122

315 KQAPMSKSPQGFATPRVYKPAPTYKSLSTSHSLKKK-----VAPFL 358

RESULT 11

A36911

glutamine synthetase I - Pyrococcus woesei

C/Species: Pyrococcus woesei

C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A36911

R/Tiboni, O.; Cammarano, P.; Sangelantoni, A.M.

U. Bacteriol. 175, 2961-2969, 1993

A/Title: Cloning and sequencing of the gene encoding glutamine synthetase I from the arch

etase I sequences.

A/Reference number: A36911; PMID:9325940; PMID:8098326

A/Accession: A36911

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-439 <TIB>

A/Cross-references: UNIPROT:P36687; GB:X60161; NID:g311383; PIDN:CAA42730.1; PID:g311384

A/Note: sequence extracted from NCBI backbone (NCBI:131878; NCBI:131879)

C/Superfamily: glutamate-aminonia ligase

Query Match 5.3%; Score 93; DB 2; Length 439;

Best Local Similarity 23.2%; Pred. No. 5.6; Matches 39; Conservative 23; Mismatches 44; Indels 62; Gaps 8;

131 PAWTLILGGSGSKPDVIPPIDP-----PPTGKTCPPAIWSLEVEY 179

308 PAFW-----GKARIEIRCPDPSANPFAFAAVAKALDGLKKHIDFFA-VYENNYE 359

180 PPTKN-----EWPYNAVELQPREFDVALKDLG-----NTKRWDSRLSYTT 224

360 MSEKKKKEGLITLPSLGEA--LEELKQKVYKELGDAYKNFNIYKKEWESYLEYL- 416

225 FRGCRNGYIDDATYLATDQMRDQKDIRGKKGAGNTERFTYL 272

417 -----EKKHMPKOTKVTEN-ELERYFPL 439

RESULT 12

A40213

optic lobe development omb protein - fruit fly (Drosophila melanogaster).

N/Alternate names: omb protein

C/Species: Drosophila melanogaster

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A40213; S34827

R/Pflugfelder, G.O.; Roth, H.; Poock, B.; Kercher, S.; Schwarz, H.; Jonscher, B.; Heise

Proc. Natl. Acad. Sci. U.S.A. 89, 1199-1203, 1992

A/Title: The lethal(1)optomotor-blind gene of Drosophila melanogaster is a major organizer

A/Reference number: A40213; PMID:92159016; PMID:1741374

A/Accession: A40213

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-974 <PFL>

A/Cross-references: UNIPROT:Q24432; GB:M81796; NID:g158018; PIDN:AAA28736.1; PID:g158019

A/Note: sequence extracted from NCBI backbone (NCBI:82056)

R/Poock, B.; Balles, U.; Pflugfelder, G.O.

Mol. Gen. Genet. 238, 325-332, 1993

A/Title: Transcript identification in the optomotor-blind locus of Drosophila melanogaster

A/Reference number: S34827; PMID:93261414; PMID:8492800

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A:Accession: S34827
A:Molecule type: DNA
A:Residues: 1-447 <POE>
A:Cross-references: GB:S61732; NID:g402317; PIDN:AAB26697.1; PID:g402318
A:Experimental source: Larva
C:Genetics:
A:Gene: FlyBase:b1
A:Cross-references: FlyBase:FBgn0000179
C:Superfamily: optic lobe development omb protein; T-box homology
C:Keywords: DNA binding
F:337-521/Domain: T-box homology <TBX>

Query Match      5.3%; Score 93; DB 1; Length 974;
Best Local Similarity 21.6%; Pred. No. 16;
Matches 50; Conservative 15; Mismatches 80; Indels 86; Gaps 7;

QY    9 LGATGKGKQTLYLNPRGVNFTNGVASLSQAGVPALEKRYTVSVSQSPRRKRKYQVK 68
Db     529 MSNNGSDDSK---LNPRTVSSSRAPLHLGHAGRPHLLPAAALDNOODDDDKLLDVVGR 585
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   69 IQNP-----TACTANGSCDPETVTRQAY 90
Db     586 PQSLPLPLSHLQQMHAHQSAALAAMPNLHLAGAGASERAAAAAAAASAEIDLRRRLQ 645
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   91 ADVTF-----SFTQYSTDEERRAFVTELAALLASPLLIDAIDQLNP 131
Db     646 ADAADVERDGSDSCSESVGSGTGGAFRPTSTGSPKEAVGAIAAAAAAAG-----LNF 696
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  132 AYMWLLTAGGGSSGKKPDVIP-DPPIDPPRGTKYTCGFALWSIEVEYERP 181
Db     697 -----GGGSTPSPNISVGVPPIHPSPLLPFLPYHG-----YPPP 731
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY	211	TKRWMDSLSTYTERGCGKNG---	YIDLDYATDQMRCKYDKIDREGKKKGAGN	266
Db	670	SLWVGSGSLRFTT-----	NGLKEHYVRDVGFIASVQALGIVYLVNRYKGGN	717
QY	267	ERFITYLKSNAYCSLDIAAYHADVIVG	235	
Db	718	---FLARYGGFQAVAA--ASHYENGIGIFG	740	

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RESULT 14
A85607
Hypothetical protein tera [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Date: 16-Feb-2001 #sequence _revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85607; B85658
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
  Miller, L.; Grobleck, E.J.; Davis, N.W.; Lin, A.; Dimalanta, B.; Potamousis, K.; Apodaca,
  Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85607
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-385 <STO>
A:Cross-references: UNIPROT:O8X9Q4; GB:AE005174; NID:G12513977; PIDN:AAG5317.1; GSPDB:GN
  A:Experimental source: strain O157:H7, substrain EDL933
A:Accession: B85658
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-385 <ST2>
A:Cross-references: GB:AE005174; NID:G12514497; PIDN:AAG55726.1; GSPDB:GN00145; UWGP:Z161
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: tera, tera_2

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	117	154	155	631	632	669
Qy	LASPLLDALIQNALPMTLLIAGS-----GSGS---KEDPVTPDP	154	-----GSGS---KEDPVTPDP	631	-----GSGS---KEDPVTPDP	669
Db	YDNPLFNMAVLIPTVTLISQTTGGVTTSAVTLNNADTAHGYGSGMSADMRPPPLADP	631	-----GSGS---KEDPVTPDP	631	-----GSGS---KEDPVTPDP	669
Qy	-----PIDPPPTGKYTCFPAIWSLEVEYEPPTKRPMPPIYNAVLEQREPDVALKDLGN	210	-----PIDPPPTGKYTCFPAIWSLEVEYEPPTKRPMPPIYNAVLEQREPDVALKDLGN	210	-----PIDPPPTGKYTCFPAIWSLEVEYEPPTKRPMPPIYNAVLEQREPDVALKDLGN	210
Db	632	669	669	669	669	669

DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: E90696
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1461 <HAY>
A:Cross-references: UNIPROT:O6XD19; GB:BA000007; PIDD:BAE33964.1; PID:G13359999; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs0541

Query Match 5.2%; Score 91.5; DB 2; Length 1461;

Best Local Similarity 21.1%; Pred. No. 36;

Matches 72; Conservative 40; Mismatches 144; Indels 85; Gaps 14;

```
QY 13 GKDGRKTLVNPGRGVPPTNGVSLSQAVPALEK---RVTVSVSQP-----SRNRK 61
Db 856 GNTGSQSLTVTVTAAPLIGINSIAGDDVINASEKGADLQITGTSDQPVNTAITVTIANQ 915
QY 62 NYKVQVKIGN-----PTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVTELA 114
Db 916 NYTTTDSAGNMSVTVPASAVTALGQANTVT---AAVTSDIGNSATASHNVLDALP 971
QY 115 ALIASPLLDALDOLNPAYWTLIIAGSGSGSKPDPIPPIDPPPGTKYTCFPAIWSL 174
Db 972 GVTINPVATDDIINAEAGVAGTISQVGAEDGDT---VTTLGNTYTATVG----- 1022
QY 175 EEVYEPTKRPWPFIYNNAVELQPREFDVALKDI--LGNTKMRPMDSRSLSTTFRGCRNG 232
Db 1023 -----SNLTWSV-----DVPADIQALGN---GDLTVNASVTNONGNTGSG 1060
QY 233 ----YIDLATYATQAMRDQKYDIIE-----GKKPG-----AFGNIRFIY 271
Db 1061 TRDITIDANPGIRVTVAGDDVNVIIIEGQALVTGSSGLAESTPLTVTINNVE---Y 1117
QY 272 LKSINAYCSLS-----DIAAYHADGVIVGFWRDPSSGAI 306
Db 1118 TTAIVQADGSWSVGVTAAQVSAWPAAGTVNTIIVSGESSAGNSV 1158
```

Search completed: January 4, 2005, 09:17:28
Job time : 21.8066 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 90.3943 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-4
Perfect score: 1749
Sequence: 1 MAKETVTLGNIGKDGKQTL.....FTKPKTKPCIPQAVIVPRA 329

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	100.0	329	2	Q8LTEL bacterioph
2	1749	100.0	329	2	AAA16663 bacteri
3	1362	77.9	329	2	O64307 enterobacte
4	1343	76.8	329	2	O64303 bacterioph
5	983	56.2	331	1	VA1_BRSP bacteri
6	897.5	51.3	330	2	O64310 enterobacte
7	668	38.2	133	2	AAA33126 bacteri
8	663	37.9	132	1	COAT_BPOBE bacteri
9	577	33.0	133	2	O9TOR9 enterobacte
10	557	31.8	133	2	O9TOR8 enterobacte
11	542.5	31.0	132	1	COAT_BRSP bacteri
12	506.5	29.0	132	2	O9TOR8 enterobacte
13	118	6.7	329	2	O66157 streptomyc
14	117	6.7	131	1	COAT_BPPRR bacteri
15	113.5	6.5	409	2	O91YZ7 sulfolobus
16	107	6.1	353	2	O919P4 brachydanio
17	106	6.1	473	2	O8VDC2 mus musculi
18	106	6.1	973	2	O86728 streptomyc
19	104	5.9	803	2	O6TDS3 oryza sativ
20	104	5.9	803	2	AAQ9280 oryza sat
21	100	5.7	955	2	O92625 salmonella
22	100	5.7	955	2	O7CRG9 salmonella
23	98	5.6	785	2	O8ZTV7 pyrobaculum
24	98	5.6	1197	2	O6P9Q4 mus musculi
25	98	5.6	1197	2	O8BMR2 mus musculi
26	98	5.6	1197	2	AAH0654 mus musculi
27	97	5.5	1426	2	O9X3P6 caldicellul
28	95.5	5.5	1326	2	O9HYU6 pseudomonas
29	95.5	5.5	1365	2	O37174 bamboo mosa
30	95	5.4	1365	2	O65005 bamboo mosa
31	94.5	5.4	530	1	TACY_LRSSSE listeria se

32	94.5	5.4	530	2	AA97361	AA97361 listeria
33	94.5	5.4	810	2	O944W5	O944W5 oryza sativ
34	94	5.4	501	1	GDPS_HUMAN	P43026 homo sapien
35	94	5.4	905	1	VP3_AHSV4	P32509 african hor
36	93.5	5.3	540	2	O48683	O48683 arabidopsis
37	93.5	5.3	552	2	O8X045	O8X045 neurospora
38	93.5	5.3	978	2	O7TQ63	O7TQ63 mus musculi
39	93.5	5.3	1249	2	O8CHH2	O8CHH2 mus musculi
40	93	5.3	439	1	GLNA_PYRPU	O05907 pyrococcus
41	93	5.3	439	1	GLNA_PYRMO	P36687 pyrococcus
42	93	5.3	972	1	OMB_DROME	O24432 drosophila
43	93	5.3	4382	2	O6TH39	O6TH39 sars corona
44	93	5.3	4382	2	O6TH47	O6TH47 sars corona
45	93	5.3	4382	2	O6R7Y7	O6R7Y7 sars corona

ALIGNMENTS

RESULT 1									
ID	Q8LTEL	PRELIMINARY;	PRT;	329 AA.					
AC	Q8LTEL								
DT	01-OCT-2002 (T-EMBLrel. 22, Created)								
DT	01-OCT-2002 (T-EMBLrel. 22, Last sequence update)								
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)								
DE	A1 read-through protein (A1 protein).								
OS	Bacteriophage Q-beta.								
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;								
OC	Allolevivirus.								
OX	NCBI_TaxId=12009;								
RN	(1)								
RP	SEQUENCE FROM N.A.								
RX	PubMed=14667253;								
RA	Bacher J.M., Bull J.J., Ellington A.D.;								
RT	"Evolution of phage with chemically ambiguous proteomes.";								
RL	BMC Evol. Biol. 3:24-24(2003).								
RN	(2)								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=94109687; PubMed=7506687;								
RA	Kozlovskaya T.M., Cielens I., Dreilinn D., Dislers A., Baumanis V.,								
RT	Ose V., Pumpens P.;								
RL	"Recombinant RNA phage Q beta capsid particles synthesized and self-								
DR	assembled in Escherichia coli.";								
DR	Gene 137:133-137(1993).								
DR	EMBL; AY099114; AAM33127.1; -.								
DR	EMBL; M99039; AAA16663.1; -.								
DR	HSSP; P03615; 1QBE.								
DR	GO; GO:0019028; C:Viral capsid; IEA.								
DR	GO; GO:0005198; P:Structural molecule activity; IEA.								
DR	InterPro; IPR002703; LevI_coat.								
DR	InterPro; IPR000504; RNA_rec_mot.								
DR	Pfam; PF01819; LevI_coat; 1.								
DR	PROSITE; PS00030; RNP_RNP_1; UNKNOWN_1.								
SQ	SEQUENCE 329 AA; 36134 MW; E0F30215A6C197CB CRC64;								
Query Match 100.0%; Score 1749; DB 2; Length 329;									
Best Local Similarity 100.0%; Pred. No. 4.6e-133;									
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAKETVTLGNIGKDGKQTLVLPNGVNPNTNGVSLSGAGVPALEKRVTVSVSQPSRRR	60						
DB	1	MAKETVTLGNIGKDGKQTLVLPNGVNPNTNGVSLSGAGVPALEKRVTVSVSQPSRRR	60						
QY	61	KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERRAFVTELLALLASP	120						
DB	61	KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERRAFVTELLALLASP	120						
QY	121	LIIDAIIDQNPAYWTLTLAGGSSGSKPDVYIDPPIIDPPGKXTCPFAISLEVEYEP	180						
DB	121	LIIDAIIDQNPAYWTLTLAGGSSGSKPDVYIDPPIIDPPGKXTCPFAISLEVEYEP	180						
QY	181	PTKRRWPPIYNAVELQPREEDVALXDLGNTKMRDMSRLSYTTRPGCGNGYIDLDATY	240						

```

Db      181 PTKRPMPIYNAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLDATY 240
Qy      241 LATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 300
Db      241 LATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 300
Qy      301 SSGGAIPEPFTKPKTCPIQAVIVPRA 329
Db      301 SSGGAIPEPFTKPKTCPIQAVIVPRA 329

```

RESULT 2

```

AAAA6663 PRELIMINARY; PRT; 329 AA.
AC 064307;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; Pubmed=7506687;
RA Kozlovskaya T.M., Clemons I., Dreilima D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli."
RL Gene 137.133-137(1993).
DR EMBL: M99039; AAA16663.1;
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

```

```

Query Match      100.0%; Score 1749; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.6e-133;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAKLEVTTLGNIGDKGKOTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRNR 60
Db      1 MAKLEVTTLGNIGDKGKOTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRNR 60
Qy      61 KNYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASP 120
Db      61 KNYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASP 120
Qy      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 180
Db      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 180
Qy      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 180
Db      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 180
Qy      181 PTKRPMPIYNAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLDATY 240
Db      181 PTKRPMPIYNAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLDATY 240
Qy      241 LATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 300
Db      241 LATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 300
Qy      301 SSGGAIPEPFTKPKTCPIQAVIVPRA 329
Db      301 SSGGAIPEPFTKPKTCPIQAVIVPRA 329

```

RESULT 3

```

AC 064307; PRELIMINARY; PRT; 329 AA.
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage X1.

```

```

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; Pubmed=7723040;
RA Beekwilder J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; Pubmed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF059242; AAC14700.1; -.
DR HSSP: P03615; 10BE.
DR GO: 0019028; C: viral capsid; IEA.
DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR002703; Lev1_coat.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF01819; Lev1_coat; 1.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

```

```

Query Match      77.9%; Score 1362; DB 2; Length 329;
Best Local Similarity 76.4%; Pred. No. 9.1e-102;
Matches 253; Conservative 26; Mismatches 46; Indels 6; Gaps 2;

```

```

Qy      1 MAKLEVTTLGNIGDKGKOTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRNR 60
Db      1 MAKLEVTTLGNIGDKGKOTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRNR 60
Qy      61 KNYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASP 120
Db      61 KNYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASP 120
Qy      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 177
Db      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 177
Qy      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 177
Db      121 LLIDAIQINLPAYWTLIIAGGSGSKDPVYIPDPPIPPPGTKYTCPPAIVSLSEYER 177
Qy      178 YEPPTKRPMPYINAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLD 237
Db      178 YEPPTKRPMPYINAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLD 237
Qy      178 YEPPTKRPMPYINAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLD 237
Db      178 YEPPTKRPMPYINAVELQPREFDVALKDLGNTKMRDSDSLSTTFRCGNGYIDLD 237
Qy      238 ATYLATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 297
Db      238 ATYLATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 297
Qy      238 ATYLATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 297
Db      238 ATYLATQAMRDQKDIIRGGKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGVWRDP 297
Qy      298 RDPSSGGAIPPEPFTKPKTCPIQAVIVPRA 328
Db      298 RDPSSGGAIPPEPFTKPKTCPIQAVIVPRA 328

```

RESULT 4

```

AC 064303; PRELIMINARY; PRT; 329 AA.
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus.
OX NCBI_TaxID=74336;
RN [1]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917 (1995).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19 (1996).
 RN
 RP SEQUENCE FROM N.A.
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF052431; AAC06251.1; -.
 DR HSPF; P03615; IQBE.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; P:structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi_coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Levi_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 329 AA; 35893 MW; 3E33CD821EB625F4 CRC64;
 Query Match 76.8%; Score 1343; DB 2; Length 329;
 Best Local Similarity 76.6%; Pred. No. 3.1e-100; Matches 252; Conservative 21; Mismatches 54; Indels 2; Gaps 2;
 QY 1 MAKLEVTLTGNIKGKQKQTLVLPNGVNPNTNGVASISQAGVAPALKEKRYTVSVSOPSRNR 60
 DB 1 MAKLGVTITSGIGKGDVTLTDLNPRGVNPTNGVAAISGAVPALKEKRYTITISVSPSRNR 60
 QY 61 KNYKQVKIQNTPACTANGSCDPSVTRQAYADYTSFTQYSDIEERAFVTELAALLASP 120
 DB 61 KNYKQVKIQNTPACTANGSCDPSVTRQAYADYTSFTQYSDIEERAFVTELAALLASP 120
 QY 121 LVIDAIDQNPAYW-TLLIAGGSGSKDP-VIPDPPIIDPPPGTKTCPEALWSLEVEYE 179
 DB 121 MIVNALIDNINPAWYAL-L-GVSGSPSPGPPDPPEPPPGTGYTCPEALWLSVYE 179
 QY 180 PPTKRRPMPPIYNAVELQPREFVALKDLGNTKWRDMSRLSTYTRGCRGNGYIDLDAI 239
 DB 180 AANSSHSWIIYNAVELSPNFDVALLDGLGNTWRMDGRLKRTTRGCRGNGYIDLDAI 239
 QY 240 YLATDQAMDQKYDIREGKKPGAFGNIERFIYKLSINAYCSLSIDIAAHADGYTVGFWRD 299
 DB 240 SLMKDEYLTSSKYLVEGRKPGVFGNIEFVYLYKSINAYCSLSIDIAHYTDGVIYVGFWRD 299
 QY 300 PSSGGAIPDFFTKEDTKCPIQAVIVPR 328
 DB 300 PSSGGAIPDFENFDSNKCPIQAVIVPR 328
 RESULT 5
 VAL_BPSP STANDARD; PRT; 331 AA.
 AC P09677;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, last sequence update)
 DT 29-MAR-2004 (Rel. 43, last annotation update)
 DE Readthrough protein A1 [contains: Coat protein].
 OS Bacteriophage SP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allotlevivirus.
 OX NCBI_TaxID=12027;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289362; PubMed=3399390;
 RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
 RT "Analysis of the complete nucleotide sequence of the group IV RNA

RT coliphage SP.";
 RL Nucleic Acids Res. 16:6205-6221 (1988).
 CC -1- FUNCTION: Not yet known.
 CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
 protein sequence.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X07489; CAB37299.1; -.
 DR PIR; S01964; S01964.
 DR HSPF; P03615; IQBE.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat; 1.
 KW Coat protein.
 FT CHAIN 1 132 Coat protein.
 FT 1 331 Readthrough protein A1.
 SQ SEQUENCE 331 AA; 36203 MW; 4A6642B4B52C6582 CRC64;
 Query Match 56.2%; Score 983; DB 1; Length 331;
 Best Local Similarity 58.5%; Pred. No. 4.1e-71; Matches 197; Conservative 45; Mismatches 77; Indels 18; Gaps 9;
 QY 1 MAKLEVTLTGNIKGKQKQTLVLPNGVNPNTNGVASISQAGVAPALKEKRYTVSVSOPSRNR 60
 DB 1 MAKLGVTITSGIGKGDQTLTLPNGVNPNTNGVAAISGAVPALKEKRYTVSAQSPSRNR 60
 QY 61 KNYKQVKIQNTPACTANGSCDPSVTRQAYADYTSFTQYSDIEERAFVTELAALLASP 120
 DB 61 KNYKQVKIQNTPACTANGSCDPSVTRQAYADYTSFTQYSDIEERAFVTELAALLASP 119
 QY 121 LVIDAIDQNPAYW-TLLIAGGSGSKDP-VIPDPPIIDPPPGTKTCPEALWSLEVEYE 175
 DB 121 LVIDAIDNINPAWYAL-LIAGSGGSDNPDPPVPPD-VKPPDGTGKCEPACRYRG 177
 QY 176 EYEPPTKRRPMPPIYNAVELQPREFVALKDLGNTKWRDMSRLSTYTRGCRGNG 232
 DB 176 SIYEVKESGP-DIYERGEVSVTFDYALEDFLGNTMNMWQRLSDYDIANRRRCRGNG 236
 QY 233 YIDLATYATQAMDQKYDIREGKKPGAFGNIERFIYKLSI--NAYCSLSIDIAHYAD 290
 DB 237 YIDLATIAQSDDFVLSGRYGVKAFGAFSGSIK---YLLNIQSDAWLDSLSEVTRYRSY 293
 QY 291 GVIVGFWRDPSSGGAIPDFFTKEDTKCPIQAVIVPR 327
 DB 294 GNVIVGFWRD-SKSPQLPTDFTQFNSANCPVQTVIITP 329
 RESULT 6
 ID 064310 PRELIMINARY; PRT; 330 AA.
 AC 064310;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, last annotation update)
 DE A1-protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allotlevivirus.
 OX NCBI_TaxID=75725;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917 (1995).
 RN

RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RL Control of A-protein synthesis.";
 RT J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSP; P03615; IQBE.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Levi_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 330 AA; 36175 MW; 961855F408334410 CRC64;

Query Match 51.3%; Score 897.5; DB 2; Length 330;
 Best Local Similarity 54.5%; Pred. No. 3.3e-64;
 Matches 181; Conservative 46; Mismatches 96; Indels 9; Gaps 7;

QY 1 MAKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRR 60
 DB 1 MAKLNVTITGIGKAGNQTLTLPRGVNPPTNGVASISBAGAVPALEKRVTVSVSQPSRR 60
 QY 61 KNTKVVQKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERRAFRTETLALLASP 120
 DB 61 KNTKVVQKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERRAFRTETLALLASP 119
 QY 121 LLIDAIDQINPAYW-TLLTAGGGSGSKDPVPIPDPP-IDPPGTGKYTCFPAIWSLEEVY 178
 DB 120 LLIDAIDQINPAYW-TLLTAGGGSGSKDPVPIPDPP-IDPPGTGKYTCFPAIWSLEEVY 179
 QY 179 EPTTKNRPMPIYNAVELOPREFDVALKDLGNTKMRDMSRLS---YTFRGCRNGGYID 235
 DB 180 -TEAKDGAQCALVCGSEBALVEFYALBEDFLGNEFMNMDRLSKYDIEHRRCRKNGGYD 238
 QY 236 LDATYTLATDQAMDQKYDIREGKKPGAFGNTERTFYKSLNAYCSLDIAHYADQVYIG 295
 DB 239 LDASVWQSGSEYVLSGAYDVVKQMPGTFDPSRYTLHMD-GIYVDLAETVAARYSYGVWIG 297
 QY 296 FWRDPSSGAIPEPDKEDTKCPQAVIYVP 327
 DB 298 FWTDD-SKSPQLPTDFTRFNHNCPCVQTVIYIP 328

RESULT 7

AA033126 PRELIMINARY; PRT; 133 AA.
 AC AA033126;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviruses; Alloviridae subgroup III.
 OX NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Becher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes.";
 RL BMC Evol. Biol. 3:24-24(2003).
 DR EMBL; AY099114; AA033126.1; -.
 KW Coat protein.
 SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 38.2%; Score 668; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.9e-46;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRR 60
 DB 1 MAKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASISBAGAVPALEKRVTVSVSQPSRR 60
 QY 61 KNTKVVQKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERRAFRTETLALLASP 120
 DB 61 KNTKVVQKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERRAFRTETLALLASP 120
 QY 121 LLIDAIDQINPAY 133
 DB 121 LLIDAIDQINPAY 133

RESULT 8

COAT_PROBE
 ID COAT_PROBE STANDARD; PRT; 132 AA.
 AC P03615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviruses.
 OX NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94109687; PubMed=7506687;
 RA Kozlovskaya T.M., Clemons I., Dreilina D., Dislers A., Baumanis V.,
 RA Ose V., Pumpens P.;
 RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
 RT assembled in Escherichia coli.";
 RL Gene 137:133-137(1993).
 RN [2]
 RP SEQUENCE OF 1-80 FROM N.A.
 RX MEDLINE=79048469; PubMed=361741;
 RA Escarria C., Sastre P.A., Billeter M.A.;
 RT "Determination of the first half of the coat protein cistron of
 RT bacteriophage Q-beta as an application of a mapping procedure for RNA
 RT fragments.";
 RL J. Biol. Chem. 253:8390-8399(1978).
 RN [3]
 RP REVISIONS TO 1-60.
 RX MEDLINE=7118573; PubMed=838709;
 RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
 RT "Revised amino acid sequence of Qbeta coat protein between positions 1
 RT and 60.";
 RL J. Biol. Chem. 252:990-993(1977).
 RN [4]
 RP SEQUENCE.
 RX MEDLINE=71288580; PubMed=5570434;
 RA Watta T., Konigsberg W.;
 RT "The amino acid sequence of the Q-beta coat protein.";
 RL J. Biol. Chem. 246:5003-5024(1971).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
 RX MEDLINE=96347354; PubMed=876553;
 RA Golmohammadi R., Fridory K., Bundale M., Valgard K., Liljas L.;
 RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
 RL Structure 4:543-554(1996).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 CC -----
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 CC -----
 DR EMBL; M99039; AAA16662.1; -.

QY 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTSEFTQYSTDEBRAPVTELTALLASP 120
 DB 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTSEFTQYSTDEBRAPVTELTALLASP 120
 QY 121 LVIDAIDQINPAY 133
 DB 121 LVIDAIDQINPAY 133

RESULT 11
 COAT BRSP STANDARD; PRT; 132 AA.
 ID COAT BRSP
 AC P09673;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Coat protein.
 OS Bacteriophage SP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allovirvirus.
 NCBI_TaxID=12027;
 RX MEDLINE=88289362; PubMed=3399390;
 RA Hiraehina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
 RT "Analysis of the complete nucleotide sequence of the group IV RNA
 coliphage SP."
 RL Nucleic Acids Res. 16:6205-6221(1988).
 CC -FUNCTION: Forms the phage shell; binds to the phage RNA.
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 CC
 CC EMBL; X07489; CA130374.1; -.
 DR HSSP; P03615; IOBE.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein; RNA-binding.
 SQ SEQUENCE 132 AA; 14129 MW; 50B1B6CC6AF0A254 CRC64;

Query Match 31.0%; Score 542.5; DB 1; Length 132;
 Best Local Similarity 79.7%; Pred. No. 5,4e-36;
 Matches 106; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSSNR 60
 DB 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSSNR 60
 QY 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTSEFTQYSTDEBRAPVTELTALLASP 120
 DB 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTSEFTQYSTDEBRAPVTELTALLASP 120
 QY 121 LVIDAIDQINPAY 133
 DB 121 LVIDAIDQINPAY 133
 QY 120 LVIDAIDQINPAY 132

RESULT 12
 COAT BRSP PRELIMINARY; PRT; 132 AA.
 ID COAT BRSP
 AC P09708;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteria phage NU95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC Allovirvirus.
 OX NCBI_TaxID=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phase Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF059243; AAC14703.1; -.
 DR HSSP; P03615; IOBE.
 DR GO; GO:0019028; Cytoral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein.
 SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 29.0%; Score 506.5; DB 2; Length 132;
 Best Local Similarity 75.9%; Pred. No. 4,4e-33;
 Matches 101; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSSNR 60
 DB 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSSNR 60
 QY 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTSEFTQYSTDEBRAPVTELTALLASP 120
 DB 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTSEFTQYSTDEBRAPVTELTALLASP 120
 QY 121 LVIDAIDQINPAY 133
 DB 121 LVIDAIDQINPAY 132

RESULT 13
 ID 066157 PRELIMINARY; PRT; 329 AA.
 AC 066157;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Deduced dNDP-hexose 4,6-dehydratase.
 GN Name=kaad;
 OS Streptomyces kasugaensis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1946;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M338-M1.
 RX MEDLINE=98250958; PubMed=9589071;
 RA Ikono S., Tsuji T., Higashide K., Kinoshita N., Hamada M., Hori M.;
 RT "A 7.6 kb DNA region from Streptomyces kasugaensis M338-M1 includes
 some genes responsible for kasugamycin biosynthesis.";
 RL J. Antibiot. 51:341-352(1998).
 DR EMBL; AB005901; BA25656.1; -.
 DR HSSP; P27830; IBXK.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0016857; P:carboxylate and epimerase activity, acting on . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.

DR InterPro; IPR001509; Epimerase_Dh.
 DR InterPro; IPR008089; Nuc_sugar_epim.
 DR Pfam; PF01370; Epimerase; 1.
 DR PRINTS; PRO1713; NUCEPIMERASE.
 SQ SEQUENCE 329 AA; 35600 MW; 58A0D0354BD36FF4 CRC64;

Query Match 6.7%; Score 118; DB 2; Length 329;
 Best Local Similarity 26.0%; Pred. No. 0.36;
 Matches 52; Conservative 29; Mismatches 91; Indels 28; Gaps 8;

QY 16 GROTIVLNRGVNPNGVSLSQAGV-VALERKVTYVSQSPRNKNK----- 64
 DB 10 GQOVLTGADFTGSHLTETLVSRGARVAVVR--VSAQVTHRLNLSAATDALERV 67
 QY 65 VQVKIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDERRAFVTELAALLASPLID 124
 DB 68 VAVDLAGEPAVAVVGRLEADTWPHLAAD---AVPMSLDQPADVVTNMTSLH---VLL 121
 QY 125 AIDQINPAYWTLILAGGSGSKPDVTPPPIDP--PQTKKTCFPAIWSLEEYVE-PP 181
 DB 122 AAQOQOPAHILVTSSEEVGSDPADITERHPLPATPYAASKVACDRLAMSWHHTYGLPL 181
 QY 182 TKNRPW-----PIYNAVEL 195
 DB 182 TIVRPENSTYGRPHVYDAVPL 201

RESULT 14
 COAT_BPPRR STANDARD; PRT; 131 AA.

AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein. PRR1.
 OS Bacteriophage PRR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OC NCBI_TaxId=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.,
 RT "The primary structure of the coat protein of the broad-host-range RNA
 RT bacteriophage PRR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR PIR; A04225; VCBPPI.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KM Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7E639E1E50FC12 CRC64;

Query Match 6.7%; Score 117; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.14;
 Matches 42; Conservative 15; Mismatches 57; Indels 16; Gaps 5;

QY 18 QTLVNLPRGVNPT-----NGVASLSQAGAVALKRKYVSQSRRKRYKVOV 67
 DB 4 QNLVTKDRATPNDHTFVRDIRDNGEYVESGVPIGSRFTISLRKTSNGR--YKSTL 61
 QY 68 KIQNPT--ACTANGSCDPSVTRQAVADYTFSTQYSTDERR-afvTELAALLASPLI- 123
 DB 62 KLVVEVVGSGTNGVITPVVATSTYTVDPDARSTTERKNNFVGMIDALKADMLVH 121
 QY 124 DAIDQINPAY 133
 DB 122 DTIVNLQGVY 131

RESULT 15
 Q97YZ7 PRELIMINARY; PRT; 409 AA.

AC Q97YZ7;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedCusNames=SS01152;
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OC NCBI_TaxId=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427126;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Dwyer M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moore A., Erasmo G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Thieriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006731; AKK41403.1; --
 DR PIR; D90268; D90268.
 DR InterPro; IPR002510; Peptidase_U62.
 DR Pfam; PF01523; Pmba_T1D; 1.
 SQ Complete proteome; Hypothetical protein.
 SQ SEQUENCE 409 AA; 46122 MW; B5AB9BC6831AA522 CRC64;

Query Match 6.5%; Score 113.5; DB 2; Length 409;
 Best Local Similarity 23.0%; Pred. No. 1.1;
 Matches 62; Conservative 36; Mismatches 99; Indels 73; Gaps 13;

QY 89 AYADVTFTQYSTDEERAFVTELAAL-----LASPL-----LIDALQINP 131
 DB 160 AFSSTSFSSQYKDSIKKA--NELASITGKXYTEGKQDVILSLVMGNLMEVARMAS 216
 QY 132 AY-----WTLILAGGSGSKPDVTPPPIDP-----PQT-----GKYTCPF 169
 DB 217 GYAIMSGSMLEKPKGKAGSDKFTLDTPEKEDPNMGFPDDEGTFYNNKAIENGVFTTFL 276
 QY 170 AIMSLEEYVE-PTNNRPMPYINAVELQPREPVALKDLG-----NTKWRDWSRLSY 222
 DB 277 LNNELSNVFKLPSTGNAGIYPTANMLEVKGEDTSFESLSGNVVFINNVM-----Y 328
 QY 223 TTFRCGRNGYIDLATYATLADQAMRDQKTIREGKRGAFENIERFIYKSIINAYCSLS 282
 DB 329 TRFQ-----NYAEGDPSTVA-----RDAVVVVRNNGNPVGIVGRVRIADNLKRI-----LK 373
 QY 283 DIAAHADGVIVGFWRPSSGSAIPEDFTK 312
 DB 374 NIVELSRERYSVRMWDAPWQ--GVYYPALVK 402

Search completed: January 4, 2005, 09:16:14
 Job time : 92.3943 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663
Sequence: 1 AKLETVTIGNIGKDGKQTLV.....AALLASPLLDIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
PIR_79:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	132	1	VCBPOB coat protein - pha
2	537.5	81.1	131	2	S01964 readthrough protei
3	117	17.6	131	1	VCBPP1 coat protein - pha
4	94.5	14.3	530	2	S22340 beeligeritolysin -
5	89.5	14.1	540	2	T00646 hypothetical prote
6	89.5	13.5	529	2	S24231 liseriolysin O pr
7	89.5	13.5	529	2	A43505 liseriolysin O pr
8	89.5	13.5	529	2	AC1100 liseriolysin O pr
9	81	12.2	130	1	AC6324 coat protein - pha
10	80	12.1	130	1	VCBPGA coat protein - pha
11	79	11.9	432	2	T31660 hypothetical prote
12	78.5	11.8	528	2	S22341 ivanolysin precurs
13	78.5	11.8	1502	1	RGHYH1 cyc1/cyp3 transcri
14	78	11.8	830	2	S57537 MKT1 protein - yea
15	77.5	11.7	136	2	C98221 hypothetical prote
16	77.5	11.7	136	2	AE3065 conserved hypotet
17	77.5	11.7	1052	2	C64221 hypothetical 114K
18	77.5	11.7	1861	2	T13845 microtubule-associ
19	76	11.5	282	2	A10186 probable iron-si
20	76	11.5	340	2	S18650 homeotic protein H
21	76	11.5	340	2	A42008 homeotic protein H
22	75.5	11.4	130	1	VCBPPR coat protein - pha
23	75.5	11.4	161	4	I55480 hypothetical natri
24	75.5	11.4	1097	2	AD2572 hypothetical prote
25	75	11.3	430	2	G88884 protein K09B1.10
26	74.5	11.2	289	2	C70400 ferredoxin oxidore
27	74.5	11.2	520	1	ACMSD1 nicotinic acetylch
28	74.5	11.2	601	2	AA5921 serine/threonine k
29	73.5	11.1	129	1	VCBPF2 coat protein - pha

30	73.5	11.1	129	1	VCBPP7 coat protein - pha
31	73.5	11.1	129	1	VCBPPZ coat protein - pha
32	73.5	11.1	384	2	A45490 neutropetide y/pep
33	73.5	11.1	719	2	T39271 conserved hypotet
34	73.5	11.1	2110	2	H96803 unknown protein T5
35	72.5	10.9	458	2	T49114 hypothetical prote
36	72.5	10.9	654	2	S63673 SAC7 protein - yea
37	72	10.9	399	1	A43685 polymerase-associa
38	72	10.9	1461	2	E30696 hypothetical prote
39	72	10.9	1461	2	A85547 hypothetical prote
40	71.5	10.8	191	2	H90078 hypothetical prote
41	71.5	10.8	683	2	AD0899 probable exported
42	71	10.7	243	1	VHVUPT nucleocapsid prote
43	71	10.7	366	2	F70618 probable putaa pro
44	70.5	10.6	130	1	VCBPM2 coat protein [vali
45	70	10.6	376	2	C84316 hypothetical prote

ALIGNMENTS

RESULT 1
VCBPOB
coat protein - phage Q-beta
C/Species: phage Q-beta
C/Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004
A/Accession: A92240; A92221; A92088; A04224
R/Bescaumis, C.; Sastry, P.A.; Biller, M.A.
J. Biol. Chem. 253, 8390-8399, 1978
A/Title: Determination of the first half of the coat protein cistron of bacteriophage Qb
A/Reference number: A92240; MUID:79048469; PMID:838709
A/Accession: A92221
A/Reference number: A92221; MUID:77118576; PMID:838709
A/Molecule type: mRNA
A/Residues: 1-80 <ESC>
A/Cross-references: UNIPROT:P03615
R/Stoll, E.; Wilson, K.J.; Reiser, J.; Weissmann, C.
J. Biol. Chem. 252, 990-993, 1977
A/Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.
A/Reference number: A92221; MUID:77118576; PMID:838709
A/Accession: A92088
A/Molecule type: protein
A/Residues: 1-60 <STO>
R/Malta, T.; Konigsberg, W.
J. Biol. Chem. 246, 5003-5024, 1971
A/Title: The amino acid sequence of the Qbeta coat protein.
A/Reference number: A92088; MUID:71288580; PMID:5570434
A/Accession: A92088
A/Molecule type: protein
A/Residues: 1-21, 'D', '23-55, 57-132 <MAI>
C/Superfamily: phage GA coat protein

Query Match 100.0%; Score 663; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTIGNIGKDGKQTLVNPGRVNPPTNGVASSQAGVPALEKRVTVSVQSPRRK 60
DB 1 AKLETVTIGNIGKDGKQTLVNPGRVNPPTNGVASSQAGVPALEKRVTVSVQSPRRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTYSTDEBERAFRTIELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTYSTDEBERAFRTIELAALLASPL 120
QY 121 LIDAIQINPAY 132
DB 121 LIDAIQINPAY 132

RESULT 2
S01964
readthrough protein - phage SP
C/Species: phage SP
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S01964
 C:Inokuchi, Y.; Jacobson, A. B.; Hirose, T.; Inayama, S.; Hiraishima, A.
 Nucleic Acids Res. 16, 6205-6221, 1988
 A:Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP
 A:Reference number: S01963; MUID:88289362; PMID:3399390
 A:Accession: S01964
 A:Status: Preliminary
 A:Molecule type: genomic RNA
 A:Residues: 1-331 <IN>
 A:Cross-references: UNIPROT:P09677; EMBL:X07489
 A:Note: the authors translated the readthrough stopcodon TGA for residue 133 as TTP
 ;Superfamily: phage GA coat protein

Query Match	81.1%	Score 537.5	DB 2	Length 331
Best Local Similarity	79.5%	Pred. No. 6.4e-45		
Matches 105, Conservative	12	Mismatches 14	Indels 1	Gaps 1

Oy

1 AKLEIYTLGNIGKDGKQTLVLPNGRVNPNGVASLSQAQAVPALEKRVTYSVSQPSRNRK 60
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db

2 AKLNYTSLSKIGNGDQLTLTPRGVNPTNGVASLSQAQAVPALEKRVTYSVAQPESRRRK 61

```

61 NYKQVQKIQNPACTANGSCSPSVTEQYADVTFSPFQYSTDEERAFRTTELAALLSPL 1200
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 NFKVQIKLQNPACTRD-ACPPSVTSFAFADVTLSFISYSTDEERALLRTTELAALLDPL 1200

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```
QY      121 LIDAIQNLNPA 132
        ::|||l|||
Db      121 IVDAILNLNPA 132
```

RESULT 3
VCBPPI
coat protein - phage PRRI

C;Date: 30-Nov-1979 #sequence 30-Nov-1979 #text_change 09-Jul-2004

R.; Dhaese, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
 Plant Dis. Rep. 74: 375-386, 1990.

A;Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage A;Reference number: A04325; MIMD:79148387; PMID:107028

A;Accession: A04225
A;Molecule type: protein

A;Cross-references: UNIPROT:P03616

C; Superfamily: phage GA coat protein

Query Match	17.6%;	Score 117;	DB 1;	Length 131;
Best Local Similarity	32.3%;	Prod NO 0	00029.	

Matches	42;	Conservative	15;	Mismatches	57;	Indels	16;	Gaps	5;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

QY 1 QILVLMRGRGVNFI-----NGVASISQAGAPFALEERKVIYSVSQPSKRNKNTAVQV 66
 ||| : : : ||| : : : ||| :
 Db 4 QNLVLKDRATENDHTFVPRDIRDNVGEVVESTGVPIGSRFTISLRKTSNGR--YKSTL 61

67 KLQNP--ACIANGSCDPSVIRQAYADVTFSTYQISIDEER-AFVKTBLEAALLSPUL- 122
| : | : | | | : | : | : | : | : | :
Db 62 KLVPEVVSQCIWGIIVTPVVRTSYTVDFDIDARSTTKERNNFVGMTADALAKADMVH 121

QY	123	DAIDQLNPAY	132
Db	122	DTIVNLQGVY	131

RESULT 4
S22340

C;Species: *Listeria seeligeri*
C;Date: 22-Nov-1993 #asmience revisi

C;Accession: S22340
R;Haab, A.; Dumbsky, M.; Kreft, J.

A;Title: Listeriolysin genes: complete sequence of *llo* from *Listeria ivanovi* and of *lsc*

A:Accession: S22340
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-530 <HAA>
A:CROSS-references: UNIRROW:P31830, EMBL:X60462, NID:G44144, PIDN:CAA42996.1, PID:G44145
A:Note: the authors translated the codon GCC for residue 287 as Pro.
i:superfamily: dipeptide transport protein

Query Match	14.3%	Score	94.5	DB	2	Length	530
Best Local Similarity	25.8%	Pred. No.	0	23			
Matches	34	Conservative	23	Mismatches	40	Indels	35
						Gaps	7

QY	13	KDGGQT	LVLT	-NPRGVNPT	-----	-NGVAST	SOAGA	-----	-VALLERK	48	
Db	94	KDGGSEIYIV	VEKKKK	GINONNAD	ISVINAT	ISLTPTG	ALVYKAN	REL	VENQPN	LVFKRDL	153

```

Qy      49 TVSVSQPSRRKKNYKVQKIQNPCTACANGSCDPSTR-----QAVDVTFTQYSTD 102
      154 TLSTVDLPGMTKDKNKIFVK--NPSTSNVNNVAVNTLVERWDKYSKAVPNINAKI-DYS-- 206
Db

```

QY	103	EERAFV	RT	ELAA	114
		:		:	
		:		:	
Db	209	DEMA	YSES	QLIA	220

RESULT 5
T00646

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Accession: T00646

; Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W. submitted to the EMRL Data Library. February 1998

A;Reference number: Z14197
A;Accession: T00646

A;Molecule type: DNA
A;status: cranslated L1011 GB/EMBL/DDB

A; Cross-references: UNIPROT:O48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g28

A;Gene: ATSP:F3I6.5

A; Introns: 14/3; 281/3; 428/3; 448/2; 483/3; 502/3
C: Superfamily: pyruvate dehydrogenase (lipoamide)

Query Match 14.18; Score 93.5; DB 2; Length 540;

Best Local Similarity 27.86; Pseud. NO. 0.23;
Matches 32; Conservative 14; Mismatches 54; Indels 15; Gaps 3;

```

QY      11  IGDGQKQTLVILNPRG--VNPPTNGVASLSQAQVPALEKRVTVSVSPDSRNRYN-YKTVQV 66
      .  :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      255 VKKEKKPNLIKNDGVNRINDTRGSLKPNQVGKPEINIKTVTSRKTPSPSKENGMKMKATK 314

```

```

QY      67  KIQNPTACTANGSCDPSVTRQAYADYTFSTQYSTDDEERA FVRELAALLASPLL 121
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db     315  KPAPMSISPOGEATPRVYKPAPTKSLSTSSLSLKKEK-----VSPLL 358

```

RESULT 6

S24231

C>Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text change 09-Jul-2004
A/Variety: strain 12067
C/Species: *Listeria monocytogenes*
Liberio/Lybil precursus - *Listeria monocytogenes* (strain 12067)

C;Accession: S24231
R;Raasmussen, O.F.; Beck, T.; Olsen, J.E.; Dons, L.; Rossen, L.

A;Title: Listeria monocytogenes isolates can be classified into two major types according to

A/Accession: S24231

A:Molecule type: DNA

A/Residues: 1-529 <RAS>
A/Cross-references: UNIPROT:P13128; EMBL:X60035; NID:G44110; PID:CAA42639.1; PID:G44112
A/Experimental source: strain 12067, serotype 4b
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C/Genetics:
A/Gene: hlyA
C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-529/Product: listeriolysin #status predicted <MNT>

Query Match 13.5%; Score 89.5; DB 2; Length 529;
Best Local Similarity 23.5%; Pred. No. 0.71;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;

QY 13 KDGRKTLV-----NPRGVNPTNGVASLSQGA-----VPALEKRV 48
DB 93 KDGEYIVVEKKKKKINONNADIQVNNAISSLITFGALVKANSELVENOPDVLVPRKDSL 152
QY 49 TVSVQSPSRNRKNRYQVQKIQNPACTANGSCDPSVTR-----QAYADVTFSTFOYSTD 102
DB 153 TLTSLDLPGMTQNDKNIIVK--NATKSNVNNNAVTLVERNKKYQAQYPRVS---AKIDVD 207

QY 103 EERAFVTELLAA 114
DB 208 DEMAYSESOLIA 219

RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C/Species: Listeria monocytogenes
C/Date: 21-Oct-1992 #sequence revision 21-Oct-1992 #text_change 09-Jul-2004
C/Accession: A43505; S05306; A47606; S12400; A61079
R/Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanrey
Interact. Immun. 56, 766-772, 1988
A/Title: Expression in Escherichia coli and sequence analysis of the listeriolysin O det
A/Reference number: A43505; MUID:88153053; PMID:3126142
A/Accession: A43505
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <MEN>
A/Cross-references: UNIPROT:P13128; GB:M24199; NID:G149652; PIDN:AAA03018.1; PID:G149653
A/Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R/Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A/Title: Nucleotide sequence of the listeriolysin gene from a Listeria monocytogenes ser
A/Reference number: S05306; MUID:8936684; PMID:2505236
A/Accession: S05306
A/Molecule type: DNA
A/Residues: 1-529 <DOM>
A/Cross-references: EMBL:X15127; NID:G44106; PIDN:CAA33223.1; PID:G44107
A/Experimental source: strain EGD
A/Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R/Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3227, 1987
A/Title: Identification of the structural gene encoding the SH-activated hemolysin of Li
A/Reference number: A47606; MUID:88057627; PMID:2824384
A/Accession: A47606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 413-480 <ME2>
A/Cross-references: GB:M29171
R/Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A/Title: Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtain
A/Reference number: S12400; MUID:91211627; PMID:1965218
A/Accession: S12400
A/Molecule type: DNA
A/Residues: 483-493 <MIC>
A/Experimental source: strain LO28, serotype 1/2c
C/Genetics:
A/Gene: hlyA; hlyA

C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-529/Product: listeriolysin O #status predicted <MNT>

Query Match 13.5%; Score 89.5; DB 2; Length 529;
Best Local Similarity 23.5%; Pred. No. 0.71;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;

QY 13 KDGRKTLV-----NPRGVNPTNGVASLSQGA-----VPALEKRV 48
DB 93 KDGEYIVVEKKKKKINONNADIQVNNAISSLITFGALVKANSELVENOPDVLVPRKDSL 152
QY 49 TVSVQSPSRNRKNRYQVQKIQNPACTANGSCDPSVTR-----QAYADVTFSTFOYSTD 102
DB 153 TLTSLDLPGMTQNDKNIIVK--NATKSNVNNNAVTLVERNKKYQAQYPRVS---AKIDVD 207

QY 103 EERAFVTELLAA 114
DB 208 DEMAYSESOLIA 219

RESULT 8
AC1100
Listeriolysin O precursor [imported] - Listeria monocytogenes (strain EGD-e)
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC1100
R/Glasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baghero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Duessegel, O.; Entian, K.D.; Psith, H.;
D.; Jones, L.M.; Karsel, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voess, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1100
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <GLA>
A/Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:G16409567; GSPDB:C
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: hly
C/Superfamily: dipeptide transport protein

Query Match 13.5%; Score 89.5; DB 2; Length 529;
Best Local Similarity 23.5%; Pred. No. 0.71;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;

QY 13 KDGRKTLV-----NPRGVNPTNGVASLSQGA-----VPALEKRV 48
DB 93 KDGEYIVVEKKKKKINONNADIQVNNAISSLITFGALVKANSELVENOPDVLVPRKDSL 152
QY 49 TVSVQSPSRNRKNRYQVQKIQNPACTANGSCDPSVTR-----QAYADVTFSTFOYSTD 102
DB 153 TLTSLDLPGMTQNDKNIIVK--NATKSNVNNNAVTLVERNKKYQAQYPRVS---AKIDVD 207

QY 103 EERAFVTELLAA 114
DB 208 DEMAYSESOLIA 219

RESULT 9
A46324
Coat protein - phage JP34
C/Species: phage JP34
A/Note: host Escherichia coli
C/Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A46324
R/Adhin, M.R.; Hirashima, A.; Van Duin, J.
Virology 170, 238-242, 1989
A/Title: Nucleotide sequence from the ssRNA bacteriophage JP34 resolves the discrepancy i

A:Reference number: A46324; MUID:89243181; PMID:2718383
A:Accession: A46324
A:Molecule type: genomic RNA
A:Residues: 1-130 <ADH>
A:Cross-references: UNIPROT:P34700; GB:J04343; NID:g215076; PIDN:AAA72210.1; PID:g215077
C:Superfamily: phage GA coat protein
C:Keywords: coat protein

Query Match 12.2%; Score 81; DB 1; Length 130;
Best Local Similarity 25.0%; Pred. No. 0.94;
Matches 35; Conservative 24; Mismatches 61; Indels 20; Gaps 5;

QY 1 AALEVTTLGNIGKDGQTLVLPNGVPTNGVA-----SLSQAGVPALEKRYTVSVSQ 54
DB 2 AATRSFVLVDNCGTGVTVV---PVSANAGVAEWLSNNSRSGA-----YKVTASVRA 50
QY 55 PSNRNRKYVQVYKIQNPACTANGSCDPSVTRQAVADVTFSPFOYSTDEERAFAVRETLAA 114
DB 51 SGADRRKXVTKLEVPKIVYQVNVGVELPVSAMKAVASIDLTIPFPAATDDVTVISKSLAG 110
QY 115 L--LASPLLDIDAIDQNPAY 132
DB 111 LFKVGNP-IADAISQSGFY 129

RESULT 10
VCBPGA
coat protein - phage GA
C:Species: phage GA
A>Note: host Escherichia coli
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29178
R:Inokuchi, Y.; Takahashi, R.; Hirose, T.; Inayama, S.; Jacobson, A.B.; Hirashima, A.
J. Biochem. 99, 1169-1180, 1986
A:Title: The complete nucleotide sequence of the group II RNA coliphage GA.
A:Reference number: A92000; MUID:86223910; PMID:3711059
A:Accession: A29178
A:Molecule type: genomic RNA
A:Residues: 1-130 <INO>
A:Cross-references: UNIPROT:P07234; GB:D10027; GB:D00046; GB:X03869; NID:g217784; PIDN:H
C:Superfamily: phage GA coat protein
C:Keywords: coat protein

Query Match 12.1%; Score 80; DB 1; Length 130;
Best Local Similarity 24.3%; Pred. No. 1.2;
Matches 34; Conservative 25; Mismatches 61; Indels 20; Gaps 5;

QY 1 AALEVTTLGNIGKDGQTLVLPNGVPTNGVA-----SLSQAGVPALEKRYTVSVSQ 54
DB 2 AATRSFVLVDNCGTGVTVV---PVSANAGVAEWLSNNSRSGA-----YKVTASVRA 50
QY 55 PSNRNRKYVQVYKIQNPACTANGSCDPSVTRQAVADVTFSPFOYSTDEERAFAVRETLAA 114
DB 51 SGADRRKXVTKLEVPKIVYQVNVGVELPVSAMKAVASIDLTIPFPAATDDVTVISKSLAG 110
QY 115 L--LASPLLDIDAIDQNPAY 132
DB 111 LFKVGNP-IADAISQSGFY 129

RESULT 11
TJ1660
hypothetical protein COS41.6 - sea equit (Cliona intestinalis)
C:Species: Cliona intestinalis
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: TJ1660
R:Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Dobson, R.; Tweedie, S.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z21049
A:Accession: TJ1660
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-432 <AIR>

A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CAB06050
C:Genetics:
A:introns: 180/2; 212/1; 229/3

Query Match 11.9%; Score 79; DB 2; Length 432;
Best Local Similarity 28.3%; Pred. No. 5.9;
Matches 30; Conservative 15; Mismatches 51; Indels 10; Gaps 5;

QY 4 ETVTLGNIGKDGQTLVLPNGVPTNGVASISQAGVPALEKRYTVSVSQPSNRKRYK 63
DB 242 DTSSEGVETKDDPGNLAENP---TPSNAREIQESVASEVLETTYVKSNIQ-EODSAYR 297
QY 64 VQVYKIQNPACTANGSCDPSVTRQAVADVTFSPFOYST-----TDRE 104
DB 298 KE-NPQNAFCPNRNGNCVINSNKTPNDSKIEIVDNSDDNTTDD 342

RESULT 12
S22341
Ivanolysin precursor - Listeria ivanovii
C:Species: Listeria ivanovii
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S22341; S36683
R:Haas, A.; Dumbsky, M.; Krett, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:Title: Listeriolysin genes: complete sequence of 110 from Listeria ivanovii and of 180
A:Reference number: S22340; MUID:92182018; PMID:1543752
A:Accession: S22341
A:Molecule type: DNA
A:Residues: 1-528 <HAS>
A:Cross-references: UNIPROT:P31831; EMBL:X60461
A>Note: the authors translated the codon ACA for residue 331 as Val
R:Krett, J.
submitted to the EMBL Data Library, July 1991
A:Reference number: S36683
A:Accession: S36683
A:Molecule type: DNA
A:Residues: 1-319, 'T', 321-528 <KRB>
A:Cross-references: EMBL:X60461
C:Genetics:
A:Gene: 110
C:Superfamily: dipeptide transport protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-528/Product: Ivanolysin #status predicted <MAT>

Query Match 11.8%; Score 78.5; DB 2; Length 528;
Best Local Similarity 22.0%; Pred. No. 8.4;
Matches 29; Conservative 23; Mismatches 45; Indels 35; Gaps 5;

QY 13 KDGKQTLV-----NPRGVNPTNGVASISQAG-----VPALERY 48
DB 92 KEGNDYIVVEKKKKKINONNADIOVINSLASTYFGALVKANSELVENQPDVLPVKRDSV 151
QY 49 TVSVQPSNRNRKYVQVYKIQNPACTANGSCDPSVTR-----QAVADVTFSPFOYSTD 102
DB 152 TLSIDLPG-GMVNDNEIVQVATKSNINDGVNTLVDRMNNKYSSEYPIIS--AKIDVD 206
QY 103 EERAFVRETLAA 114
DB 207 QEMAYSESQLVA 218

RESULT 13
RGBYH1
CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein 19672.1; protein YKR266w; regulatory protein CYC1, regulatory
C:Species: Saccharomyces cerevisiae
C>Date: 30-Sep-1991 #sequence_revision 23-Feb-1996 #text_change 12-Nov-1999
C:Accession: S59400; A1312; S15447; S05804; S15446
R:Johnson, D.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9672.
A:Reference number: S59386

A:Accession: S59400
A:Molecule type: DNA
A:Residues: 1-1502 <JONH>
A:Cross-references: EMBL:U20865; NID:g662330; PIND:AA67387.1; PID:g662331; GSPDB:GN0001
A:Experimental source: strain 5288C (AB972)
R:Peifer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
Cell 56, 291-301, 1989
A:Title: Functional dissection and sequence of yeast HAP1 activator.
A:Reference number: A13112; MUID:89106221; PMID:2643482
A:Accession: A31312
A:Molecule type: DNA
A:Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'M', 509-586, 'K', 588-882, 'N', 884-95
A:Cross-references: EMBL:J03152; NID:g171645; PIND:AAA34662.1; PID:g171646
R:Crusot, F.; Verdier, J.; Galsane, M.; Slonimski, P.P.
J. Mol. Biol. 204, 263-276, 1988
A:Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
A:Reference number: S15447; MUID:89125585; PMID:2851658
A:Accession: S15447
A:Molecule type: DNA
A:Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPIME' <CRE1>
A:Cross-references: EMBL:X13793
A:Note: The sequence is from mutant CYP1-18
C:Genetic8:
A:Gene: SGD:HAP1, CYP1, MIPS:YLR256w
A:Cross-references: SGD:S0004246; MIPS:YLR256w
A:Map position: 12R
C:Superfamily: regulatory protein HAP1, GAL4 zinc binuclear cluster homology
C:Keywords: DNA binding; heme binding; transcription regulation; zinc finger
F:1-148/Domain: DNA binding #status predicted <DNA>
F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F:64-84/Region: zinc finger CCCC motif
F:177-189/Region: glutamine-rich
F:245-445/Domain: heme binding #status predicted <HEM>
F:298-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats
F:1308-1481/Domain: activation element #status predicted <ACT>
F:1388-1481/Region: acidic
Query Match 11.8%; Score 78.5; DB 1; Length 1502;
Best Local Similarity 20.6%; Pred. No. 28;
Matches 35; Conservative 29; Mismatches 43; Indels 63; Gaps 7;
OY 23 PRGVN-PTNGVASI-----SQAGVPALEKRVTVSVS 53
DB 1278 PRGISPKDSNGLSVQPLSPFSMNQNGRTIPVPSILNTISQNGALPSLDRIITNGN 1337
OY 54 QPSRR-KNYKQVQKQP-----TACTANGCDP 82
DB 1338 LPDPSRDAFNDSTIKQMPMTSAFMANNTTIPSSITLNGMNNNGAGTANTDTISANGSALS 1397
OY 83 SVTRQAVADV-TFSFTQYSTD-EERAFVTELLAALASP-LTIDAIDQLN 129
DB 1398 TLTSQGSDBLASNSATQKPDLEDFLMONSFNGLMINPSSLVEVGGIN 1447
RESULT 14
S57537
MKTL protein - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N2302; protein YNL085w
C:Species: Saccharomyces cerevisiae
C>Date: 10-Oct-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57537; S50279; S63024; S63017; S65096
R:Solier-Mira, A.; Sait, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57537
A:Accession: S57537
A:Molecule type: DNA
A:Residues: 1-830 <SOA>
A:Cross-references: UNIPROT:P40850; EMBL:X89016; NID:g887621; PID:g887626
R:Vermet, M.; Widner, W.R.; Dimman, J.D.; Wickner, R.B.
Yeast 10, 1477-1479, 1994
A:Title: Sequence of MKTL, needed for propagation of M(2) satellite dsRNA of the L-A vir
A:Reference number: S50279; MUID:95176705; PMID:7532890
A:Accession: S50279

A:Molecule type: DNA
A:Residues: 1-29, 'G', 31-808, 'TMKTCTANTY' <VER>
A:Cross-references: EMBL:U09129; NID:g520475; PIND:AA639470.1; PID:g520476
R:Solier-Mira, A.; Sait, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63018
A:Accession: S63024
A:Molecule type: DNA
A:Residues: 1-830 <SOA>
A:Cross-references: EMBL:Z71361; NID:g1301982; PID:g1301983; MIPS:YNL085w
A:Experimental source: strain 5288C
R:Poelmann, R.; Philippen, P.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S63017
A:Molecule type: DNA
A:Residues: 569-830 <ROE>
A:Cross-references: EMBL:Z71361; MIPS:YNL085w
A:Experimental source: strain 5288C
R:Solier-Mira, A.; Sait, J.E.; Ballesta, J.P.G.; Remacha, M.
Yeast 12, 485-491, 1996
A:Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
A:Reference number: S65092; MUID:96310628; PMID:8740422
A:Accession: S65096
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-830 <SOF>
A:Cross-references: EMBL:X89016; NID:g887621; PIND:CAA61425.1; PID:g887626
C:Genetic8:
A:Gene: SGD:MKTL
A:Cross-references: SGD:S0005029; MIPS:YNL085w
A:Map position: 14L
C:Superfamily: Saccharomyces cerevisiae MKTL protein
C:Keywords: transmembrane protein
F:615-631/Domain: transmembrane #status predicted <TM>

Query Match 11.8%; Score 78; DB 2; Length 830;
Best Local Similarity 24.8%; Pred. No. 16;
Matches 25; Conservative 23; Mismatches 47; Indels 6; Gaps 3;
OY 5 TTTLGNIGKDGKQITLVNPRGVNPTNGVASISQAGVPALEKRVTVSVSOPSRRKNKYV 64
DB 301 STTLQN--DSKENYQNYQGISALRYMPVLDGKVELFVQEIYVSEBSEKNNKDGK- 356
OY 65 QVKIONPTACTANGSCDPSVTROAVADYVTFSTQSTDEER 105
DB 357 KSNLSSPSSASSASPATTVTKNASEKLYE--KSTIKYVR 395

RESULT 15
C98221
hypothetical protein AGR_L1428 (imported) - Agrobacterium tumefaciens (strain C58, Cerec
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C98221
R:Goodner, B.; Hinkle, G.; Gatlung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C98221
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:O808F3; GB:AB007870; PIND:AAK89293.1; PID:g15159127; GSPDB:GN
A:Gene: AGR_L1428
A:Map position: linear chromosome
Query Match 11.7%; Score 77.5; DB 2; Length 136;
Best Local Similarity 25.4%; Pred. No. 2.2;
Matches 30; Conservative 14; Mismatches 57; Indels 17; Gaps 3;

QY 11 IKDKQKQTLVLPNGVNPNGVNSQAGV-----PALEKRVTVSVSQPSRNR 59
| | | | | : | | : | : | :
Db 3 ISKDKQKQTESADPHWIEWVTGTISTLLVAAMPGMTAIDIRYSPEARPEIAVTGVEGQT 62
QY 60 KNYKVQVKIQNPACTA-----NGSCDPSVTRQAYADVTFSP-TQYSTDEBRAPVYTE 111
| | : | | : | | : | | : | : | :
Db 63 GQYRVKFAIHNLSTMTTAQVNVRGDLEQNGASPENADVTFDYVASESKDNGTLPFRSD 120

Search completed: January 4, 2005, 09:17:26
Job time : 9.03224 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663
Sequence: 1 AKLETVTGNIGKDKQTLV.....AALLAPLLIDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	132	1	COAT_BPOBE
2	663	100.0	133	1	AAAM33126
3	663	100.0	329	2	Q8L7E1
4	663	100.0	329	2	AA16663
5	572	86.3	133	2	Q9T0R9
6	572	86.3	329	2	Q9T0R9
7	552	83.3	133	2	Q9T0S0
8	552	83.3	329	2	Q9T0S0
9	537.5	81.1	132	1	COAT_BPS
10	537.5	81.1	331	1	VAL_BPS
11	501.5	75.6	132	2	Q9T0R8
12	501.5	75.6	330	2	Q9T0R8
13	117	17.6	131	1	COAT_BPPRR
14	95.5	14.4	473	2	Q8VDC2
15	94.5	14.3	530	1	TACY_LISSE
16	94.5	14.3	530	2	AA97361
17	93.5	14.1	540	2	Q48683
18	89.5	13.5	529	1	TACY_LISMF
19	89.5	13.5	529	2	TACY_LISMO
20	89.5	13.5	529	2	Q9L5B9
21	89.5	13.5	529	2	Q6E9A2
22	89.5	13.5	529	2	Q6E9A2
23	89.5	13.5	529	2	Q6E9A2
24	89.5	13.5	529	2	Q6E9A2
25	89.5	13.5	529	2	Q6E9A2
26	89.5	13.5	529	2	Q6E9A2
27	89.5	13.5	529	2	Q6E9A2
28	89.5	13.5	529	2	Q6E9A2
29	89.5	13.5	529	2	Q6E9A2
30	89.5	13.5	529	2	Q6E9A2
31	89.5	13.5	529	2	AA703000

32	81	12.2	129	1	COAT_BPP3	P34700 bacterioph
33	80	12.1	129	1	COAT_BPGA	P07234 bacterioph
34	80	12.1	130	2	Q9MBL2	Q9mb12 bacterioph
35	80	12.1	336	2	Q8TRF3	Q8trf3 methanosarc
36	80	12.1	1624	2	Q9V3K8	Q9v3k8 dirosophila
37	80	12.1	1637	2	Q9SRU8	Q9sr8 dirosophila
38	79	11.9	432	2	P91584	P91584 cioma inter
39	79	11.9	461	2	Q7PP73	Q7pp73 anopheles g
40	78.5	11.8	528	1	TACY_LISIV	P31831 listeria iv
41	78.5	11.8	528	2	Q6R6D9	Q6r6d9 listeria iv
42	78.5	11.8	528	2	AA97343	AA97343 listeria
43	78.5	11.8	608	2	Q84H79	Q84h79 rhodococcus
44	78.5	11.8	1502	1	CYPI_YEAST	P12351 saccharomyc
45	78	11.8	830	1	MKTI_YEAST	P40850 saccharomyc

ALIGNMENTS

RESULT 1
ID COAT_BPOBE STANDARD: PRT: 132 AA.
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae;
OK NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Ctelens I., Dreilima D., Dislers A., Baumann V.,
Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmins C., Saez P.A., Billeter M.A.;
RT "Determinant of the first half of the coat protein cistron of
bacteriophage Q-beta as an application of a mapping procedure for RNA
fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=7118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maier T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golshammadi R., Bundule M., Valgaard K., Liljae L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaboration -
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CC EMBL; M99039; AAA16662.1; -
CC EMBL; V00643; CAA23992.1; -
DR PIR; A92240; VCBPOB.
DR PDB; 1QBE; X-ray; A/B/C=1-132.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR 3d-structure; Coat protein; Direct protein sequencing; RNA-binding.
KW INIT MET 0 0
FT CONFLICT 22 22 N -> D (in Ref. 4).
FT CONFLICT 55 56 Missing (in Ref. 4).
FT STRAND 6 9
FT TURN 13 14
FT STRAND 18 27
FT TURN 28 31
FT STRAND 32 36
FT HELIX 42 44
FT STRAND 47 53
FT STRAND 56 56
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 74
FT STRAND 83 96
FT TURN 98 99
FT HELIX 102 117
FT HELIX 119 126
FT TURN 127 127
SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA572E CRC64;

Query Match 100.0%; Score 663; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,2e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
DB 1 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
QY 61 NRVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
DB 61 NRVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDALDQNPAY 132
DB 121 LIDALDQNPAY 132

RESULT 2
AAAM33126. PRELIMINARY; PRT; 133 AA.
ID AAAM33126; PRELIMINARY; PRT; 133 AA.
AC AAAM33126;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae; Alloviridae subgroup III.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
DR EMBL; AY09114; AAAM33126.1; -.
KM Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C3IDE CRC64;

Query Match 100.0%; Score 663; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2,2e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 61
QY 61 NRVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
DB 62 NRVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 121
QY 121 LIDALDQNPAY 132
DB 122 LIDALDQNPAY 133

RESULT 3
Q8LTE1 PRELIMINARY; PRT; 329 AA.
ID Q8LTE1
AC Q8LTE1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae;
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Dreilima D., Dislers A., Baumanns V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-assembled in Escherichia coli."
RL Gene 137:133-137(1993).
DR EMBL; AY09114; AAAM33127.1; -.
DR EMBL; M99039; AAA16663.1; -.
DR HSP; P03615; 1QBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 100.0%; Score 663; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 6,4e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 61
QY 61 NRVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
DB 62 NRVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 121
QY 121 LIDALDQNPAY 132
DB 122 LIDALDQNPAY 133

RESULT 4
AAA16663 PRELIMINARY; PRT; 329 AA.
ID AAA16663
AC AAA16663;
DT 02-MAR-2004 (TREMBlrel. 27, Created)

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DT 02-MAR-2004 (TREMblrel. 27, last sequence update)
DE 02-MAR-2004 (TREMblrel. 27, last annotation update)
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolevivirus.
OX NCBI_Taxid=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clelens I., Dreilima D., Dielers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL, M99039; AAA1663.1; -
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 100.0%; Score 663; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 6,4e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEVTVTGKNGKDKQKTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 ALEVTVTGKNGKDKQKTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 61
QY 61 NYKVQVKIÖNPACTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTEELAAALASPL 120
DB 62 NYKVQVKIÖNPACTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTEELAAALASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
ID Q9TOR9;
AC Q9TOR9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolevivirus.
OX NCBI_Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DB EMBL, AF059242; AAC14700.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; R:RNA_rec_mot.
DR InterPro; IPR00504; R:RNA_rec_mot.
DR PROSITE; PS00030; R:RNP 1; UNKNOWN 1.
DR PROSITE; PS00030; R:RNP 1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 86.3%; Score 572; DB 2; Length 329;
Best Local Similarity 84.1%; Pred. No. 4,4e-47;
Matches 111; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
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Query Match 86.3%; Score 572; DB 2; Length 133;
Best Local Similarity 84.1%; Pred. No. 1,5e-47;
Matches 111; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 ALEVTVTGKNGKDKQKTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 ALEVTVTGKNGKDKQKTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 61
QY 61 NYKVQVKIÖNPACTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTEELAAALASPL 120
DB 62 NYKVQVKIÖNPACTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTEELAAALADPM 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
DE A1-Protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolevivirus.
OX NCBI_Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DB EMBL, AF059242; AAC14700.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; R:RNA_rec_mot.
DR InterPro; IPR00504; R:RNA_rec_mot.
DR PROSITE; PS00030; R:RNP 1; UNKNOWN 1.
DR PROSITE; PS00030; R:RNP 1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 86.3%; Score 572; DB 2; Length 329;
Best Local Similarity 84.1%; Pred. No. 4,4e-47;
Matches 111; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
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RESULT 7
Q970S0 PRELIMINARY; PRT; 133 AA.
AC Q970S0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Coat protein. M11.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses.
OX NCBI_Taxid=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coat protein.
KW SEQUENCE 133 AA; 14198 MW; 098722E3C6CA255 CRC64;
SQ
Query Match 83.3%; Score 552; DB 2; Length 133;
Best local Similarity 81.1%; Pred. No. 1.3e-45;
Matches 107; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
QY 1 AKLETVTIGNIGKDGKQTLVLPNGVNPNGVNASLSQAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLQATITLGGIGKKDVTLDLPNGVNPNGVNASLSQAGVPALEKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTSCATSGTCDPSVTRSAVSVDTFSTQYSTVERALVTELAALADPM 121
QY 121 LIDAIIDQINPAY 132
DB 122 LVNAIDINLPAY 133
RESULT 8
Q64303 PRELIMINARY; PRT; 329 AA.
AC Q64303;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses.
OX NCBI_Taxid=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;

```

```

RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06251.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35893 MW; 3E33CD821EE625F4 CRC64;
Query Match 83.3%; Score 552; DB 2; Length 329;
Best local Similarity 81.1%; Pred. No. 3.8e-45;
Matches 107; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
QY 1 AKLETVTIGNIGKDGKQTLVLPNGVNPNGVNASLSQAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLQATITLGGIGKKDVTLDLPNGVNPNGVNASLSQAGVPALEKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTSCATSGTCDPSVTRSAVSVDTFSTQYSTVERALVTELAALADPM 121
QY 121 LIDAIIDQINPAY 132
DB 122 LVNAIDINLPAY 133
RESULT 9
COAT_BSP STANDARD; PRT; 132 AA.
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses.
OX NCBI_Taxid=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
RT -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
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CC or send an email to license@isb-sib.ch).
DR EMBL; X07489; CAA30374.1; -.
DR HSSP; P03615; IOBE.

```

DR InterPro: IPR002703; Lev1_coat.
 DR Pfam: PF01819; Lev1_coat; 1.
 KW Coat protein; RNA-binding.
 SQ SEQUENCE 132 AA; 14129 MW; 50B16CC6AFA0A254 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 132;
 Best Local Similarity 79.5%; Pred. No. 3.4e-44;
 Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPNGVSLSGAGVPALEKRYTVSVSOPSRNK 60
 DB 2 AKLNGVTLISKIGKNDQTLTLPNGVNPNGVSLSGAGVPALEKRYTVSVSOPSRNK 61
 QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
 DB 62 NFKVQIKQNPACTCRD-ACDPSVTRSAFADYTLSTSTDEERALLRTTELAALLADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADINLNPAY 132

RESULT 10

VAL_BPSP STANDARD; PRT; 331 AA.
 AC P09677;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Readthrough protein A1 [Contains: Coat protein].
 OS Bacteriophage SP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alilevirivirus.
 NCBI_TaxID=12027;

RP SEQUENCE FROM N.A.
 RX MEDLINE=88289362; PubMed=3399390;
 RA Hirschma A., Hirose T., Inokuchi Y., Jacobson A.B.;
 RT "Analysis of the complete nucleotide sequence of the group IV RNA
 RT coliphage SP.";
 RL Nucleic Acids Res. 16:6205-6221(1988).
 CC -1- FUNCTION: Not yet known.
 CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
 CC protein sequence.

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 CC or send an email to license@sib-sib.ch).

DR EMBL: X07489; CAB37299.1; -.
 DR PIR: S01964; S01964.
 DR HSSP: P03645; 10BE.
 DR InterPro: IPR002703; Lev1_coat.
 DR Pfam: PF01819; Lev1_coat; 1.
 KW Coat protein.
 FT CHAIN 1 132 Coat protein.
 FT CHAIN 1 331 Readthrough protein A1.
 SQ SEQUENCE 331 AA; 36203 MW; 4A6642B4B52C6582 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 331;
 Best Local Similarity 79.5%; Pred. No. 9.8e-44;
 Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPNGVSLSGAGVPALEKRYTVSVSOPSRNK 60
 DB 2 AKLNGVTLISKIGKNDQTLTLPNGVNPNGVSLSGAGVPALEKRYTVSVSOPSRNK 61
 QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
 DB 121 IVDADINLNPAY 132

DB 62 NFKVQIKQNPACTCRD-ACDPSVTRSAFADYTLSTSTDEERALLRTTELAALLADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADINLNPAY 132

RESULT 11

Q9TOR8 PRELIMINARY; PRT; 132 AA.
 AC Q9TOR8;
 DT 01-MAY-2000 (TRMBLrel. 13, Created)
 DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alilevirivirus.
 NCBI_TaxID=75725;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RT RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN (3)

RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF059243; AAC14703.1; -.
 DR HSSP: P03645; 10BE.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR002703; Lev1_coat.
 DR Pfam: PF01819; Lev1_coat; 1.
 KW Coat protein.
 SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 75.6%; Score 501.5; DB 2; Length 132;
 Best Local Similarity 75.8%; Pred. No. 1e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPNGVSLSGAGVPALEKRYTVSVSOPSRNK 60
 DB 2 AKLNGVTLISKIGKNDQTLTLPNGVNPNGVSLSGAGVPALEKRYTVSVSOPSRNK 61
 QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
 DB 62 NFKVQIKQNPACTCRD-ACDPSVTRSRDVTLSFTSTDEERALLRTTELAALLADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADINLNPAY 132

RESULT 12

O64310 PRELIMINARY; PRT; 330 AA.
 AC O64310;
 DT 01-AUG-1998 (TRMBLrel. 07, Created)
 DT 01-AUG-1998 (TRMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE A1-protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC AllLeviViruS.
 OX NCBI_TaxId=75725;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917 (1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19 (1996).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSSP; P03615; IQBE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1 coat.
 DR InterPro; IPR000504; RNA_Tec_mot.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 961855F408334410 CRC64;
 Query Match 75.6%; Score 501.5; DB 2; Length 330;
 Best Local Similarity 75.8%; Pred. No. 3e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKLETVTLGIGKDGKQTLVLRGVNPTNGVSLSQAGVPLERKRVYSQPSRNRK 60
 DB 2 AKLNKVLTLTGIGRAGNLTTLTRGVNPTNGVSLSEAGVPLERKRVYSVAQPSRNRK 61
 QY 61 NYKVQVQVIONPTCTANGSCDPSVTRQAVADVFPSFYQSTDEERAFVRETLAALLASPL 120
 DB 62 NYKVQVQVIONPTCTANGSCDPSVTRQAVADVFPSFYQSTDEERAFVRETLAALLASPL 120
 QY 121 LIDALDQINPAY 132
 DB 121 IVDALDQINPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PRL1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxId=12024;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhasee P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PRL1.";
 RL Eur. J. Biochem. 94:375-386 (1979).
 CC PIR; A04225; VCBPPI.
 DR InterPro; IPR002703; Lev1 coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KM Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B639E1B50FC612 CRC64;

Query Match 17.6%; Score 117; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0021;
 Matches 42; Conservative 15; Mismatches 57; Indels 16; Gaps 5;
 QY 17 QTLVLRGVNPT-----NGVASLSQAGVPLERKRVYSQPSRNRKRVQV 66
 DB 4 QNLVLRGVNPTNDHTFVPDIRNVEVSGVPIGSRFTLSLKTSNGR--YKSTL 61
 QY 67 KIQNPT--ACTANGSCDPSVTRQAVADVFPSFYQSTDEER-AFVRETLAALLASPLI- 122
 DB 62 KLVVFPVQSQTVNGLVFPVVRISYTVVDFDYARSTTKERNFVGMIADALKADLMVH 121.
 QY 123 DAIDQINPAY 132
 DB 122 DTIVNLQGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2
 AC Q8VDC2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Trm7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kise H., Darai E., Kise C., Kost-Allmova M., Klein G., Dumanaki J.P.,
 RA Imreh S.;
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3.";
 RL Mamm. Genome 13:646-655 (2002).
 DR EMBL; AJ428064; CAD20986.1; -.
 DR MGD; MGI:2446841; Trm7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 KM Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872B0E869F2A4D CRC64;
 Query Match 14.4%; Score 95.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 1.2;
 Matches 45; Conservative 17; Mismatches 46; Indels 69; Gaps 7;
 QY 5 TTTLGNIGKDGKQTLV-----LNRGVNPTNG--VASLSQAGVPLERKRVYSQPSRNRK 46
 DB 195 TATCSNIISSOPSSKRVQFQASKANPQASNPYKNDPKVCSKPPAPLPSLSKARAP 254
 QY 47 RVTVASVQPSRNRKRVQV-----KIQNPT-----ACTANGSCDPSVTRQAV--- 89
 DB 255 KATVTSNIISSRSSKQMPQASKVNPQTSPTNDPISCTSKSPSTPRLTIQQLSVY 314
 QY 90 -----ADVTFSTFYQSTDEERAFVRETLAALLASPLI 122
 DB 315 SPAPAPCTVIQWPSPPTPIDSGRADVAKENRSTKPK-----ALLSSPLYV 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE
 AC P1830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Selligeriolysin precursor (thiol-activated cytolysin).
 GN Name=Isol;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

OK NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLCC;
RX MEDLINE=92182018; PubMed=1543752;
RA Haas A., Dumbsky M., Kreft J.;
RT "Listeriolysin genes: complete sequence of 110 from *Listeria ivanovi*
and of 180 from *Listeria seeligeri*.";
RL Biochim. Biophys. Acta 1130:81-84(1992).
CC -!- FUNCTION: Sulfhydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
Cholesterol is the receptor for the binding of these toxins to
eukaryotic cell membranes.
CC -!- SIMILARITY: Belongs to the thiol-activated cytolysin family.
CC -----
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CC -----
DR EMBL; X60462; CAA42996.1; -
DR PIR; S22340; S22340.
DR HSSP; P19995; 1PFO.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PRO1400; TACTOLXSIN.
DR PRODOM; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
KW Cytolysis; Hemolysis; Lipid-binding; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 530 Seeligeriolysin.
FT SITE 485 485 Binding to cholesterol (by similarity).
SQ SEQUENCE 530 AA; 59181 MW; 416F7A4DD2029866 CRC64;

Query Match 14.3%; Score 94.5; DB 1; Length 530;
Best Local Similarity 25.8%; Pred. No. 1.7;
Matches 34; Conservative 23; Mismatches 40; Indels 35; Gaps 7;

QY 13 KDGKQTLV--NPRGVNPT-----NGVASLSQNGA-----VPALEKRV 48
DB 94 KDGSEYIVVEKKKGINONNADISVINAISLTPGALVKANRELVENQPNVLPKRDSL 153
QY 49 TVSVSQPSRNRRKRYVQVKTQNPFTACTANGSCDPSVTR-----QAYADVTFSFYQYSTD 102
DB 154 TLSDVLPQKTKKDKIFVK--NPTKSNVNNVAVNLVERWMDKYSKAYPNINAKI-DYS-- 208
QY 103 EERAFAVTELA 114
DB 209 DEMAYSESQLIA 220

Search completed: January 4, 2005, 09:16:12
Job time : 38.2676 secs

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OM protein - protein search, using SW model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663
Sequence: 1 AKLEVTYIGNIKGKQKQTLV.....ALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 356729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238ep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	132	5	ABG94233 Bacterioph
2	663	100.0	132	5	ABG80545 Bacterioph
3	663	100.0	132	6	ABR56439 Bacterioph
4	663	100.0	132	6	ABU09686 Bacterioph
5	663	100.0	132	6	ABR44542 Bacterioph
6	663	100.0	132	7	ADD24117 Bacterioph
7	663	100.0	132	7	ADJ82043 Protein f
8	663	100.0	132	7	ADK17131 Virus-11k
9	663	100.0	132	8	ADJ36300 Bacterioph
10	663	100.0	132	8	ADJ67146 Bacterioph
11	663	100.0	132	8	ADK52180 Bacterioph
12	663	100.0	328	6	ABR56440 Bacterioph
13	663	100.0	328	6	ABR44543 Bacterioph
14	663	100.0	329	5	ABG94278 Bacterioph
15	663	100.0	329	5	ABG80590 Bacterioph
16	663	100.0	329	6	ABU09687 Bacterioph
17	663	100.0	329	7	ADD24118 Bacterioph
18	663	100.0	329	7	ADJ82044 Protein f
19	663	100.0	329	7	ADK17132 Virus-11k
20	663	100.0	329	8	ADJ36301 Bacterioph
21	663	100.0	329	8	ADJ67147 Bacterioph
22	663	100.0	329	8	ADK52181 Bacterioph
23	655	98.8	132	5	ABG94316 Bacterioph
24	655	98.8	132	5	ABG94320 Bacterioph
25	655	98.8	132	5	ABG80632 Bacterioph

26	655	98.8	132	5	ABG80628 Bacterioph
27	655	98.8	132	6	ABR56455 Bacterioph
28	655	98.8	132	6	ABR56452 Bacterioph
29	655	98.8	132	6	ABU09689 Bacterioph
30	655	98.8	132	6	ABU09693 Bacterioph
31	655	98.8	132	6	ABR44555 Bacterioph
32	655	98.8	132	6	ABR44558 Bacterioph
33	655	98.8	132	7	ADD24130 Bacterioph
34	655	98.8	132	7	ADD24133 Bacterioph
35	655	98.8	132	7	ADJ82059 Protein f
36	655	98.8	132	7	ADJ82056 Protein f
37	655	98.8	132	7	ADK17144 Virus-11k
38	655	98.8	132	7	ADK17147 Virus-11k
39	655	98.8	132	8	ADJ36316 Bacterioph
40	655	98.8	132	8	ADJ36313 Bacterioph
41	655	98.8	132	8	ADJ67159 Phase Ope
42	655	98.8	132	8	ADJ67162 Phase Ope
43	655	98.8	132	8	ADK52196 Bacterioph
44	655	98.8	132	8	ADK52193 Bacterioph
45	652	98.3	132	5	ABG94318 Bacterioph

ALIGNMENTS

RESULT 1	
ABG94233	
ID	ABG94233 standard; protein; 132 AA.
XX	
AC	ABG94233;
XX	
DT	06-AUG-2003 (revised)
DT	10-DEC-2002 (first entry)
XX	
DE	Bacteriophage coat protein #1.
XX	
KW	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW	cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW	vaccine; infectious disease.
XX	
OS	Bacteriophage.
XX	
PN	WO200256905-A2.
XX	
PD	25-JUL-2002.
XX	
PF	21-JAN-2002; 2002WO-1B000166.
XX	
PR	19-JAN-2001; 2001US-0262379P.
PR	04-MAY-2001; 2001US-0286549P.
PR	05-OCT-2001; 2001US-0326998P.
PR	07-NOV-2001; 2001US-0331045P.
XX	
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.
XX	
PI	Renner WA, Bachmann M, Tlasec A, Maurer P, Lechner F, Sebbel P;
PI	Ploesek C;
XX	
DR	WPI, 2002-627351/67.
XX	
PT	Molecular antigen array used in the production of vaccines for infectious
PT	diseases.
XX	
PS	Claim 13; Page 379; 441pp; English.
XX	
CC	This invention relates to a novel ordered and repetitive antigen array
CC	used in the production of vaccines for infectious diseases. The invention
CC	also discloses a composition comprising a non-natural molecular scaffold
CC	comprising a core particle selected from a core particle of a non-natural
CC	origin and a core particle of natural origin and an organismer comprising
CC	at least one first attachment site, where the organismer is connected to
CC	the core particle by at least one covalent bond. Also disclosed is an
CC	antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunization and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 06
 CC -AUG-2003 to correct OS field.)

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.6e-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYIGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSQRNKK 60
 DB 1 AKLEVTYIGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSQRNKK 60
 QY 61 NKVGVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
 DB 61 NKVGVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 2

ABG80545

ID ABG80545 standard; protein; 132 AA.

XX ABG80545;

DT 29-AUG-2003 (revised)

DT 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta coat protein.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease; lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.

PN WO200256907-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002WO-1B000168.

PR 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0288549P.

PR 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEOEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Piossek C;
 DR WPI; 2002-636514/68.
 XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

XX Disclosure; Page 356-357; 418pp; English.

CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attaching site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array. (Updated on 29-AUG-
 CC 2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.6e-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYIGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSQRNKK 60
 DB 1 AKLEVTYIGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSQRNKK 60
 QY 61 NKVGVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
 DB 61 NKVGVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 3

ABR56439

ABR56439 standard; protein; 132 AA.
AC ABR56439;
DT 23-OCT-2003 (revised)
DT 28-JUL-2003 (first entry)
DE Bacteriophage Q-beta coat protein SEQ ID NO:10.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KM cytosolic; virucide; antibacterial; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KM antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
KM antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.
OS Bacteriophage Qbeta.
XX WO2003024480-A2.
PN
PD 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
PF
XX 14-SEP-2001; 2001US-0318967P.
PR
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA
XX Bachmann M, Storn T, Lechner F;
FI WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunising or treating tumors or infectious diseases, e.g. viral
PT infections.
PS Disclosure; Page 167-168; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antineumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC659852 and ABR56401 to ABR56599
CC represent sequences used in the exemplification of the present invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 663; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTYIGNIGKDKQKTLVIANPBGVPTNGVNASISQAGVAPALKKRYTVSVSOPSRRNK 60
DB 1 AKLETVTYIGNIGKDKQKTLVIANPBGVPTNGVNASISQAGVAPALKKRYTVSVSOPSRRNK 60
QY 61 NKVQVKIOMPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFYVTELAALLASPL 120
DB 61 NKVQVKIOMPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFYVTELAALLASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 LIDAIQDQNPAY 132
RESULT 4
ABU09686
ID ABU09686 standard; protein; 132 AA.
XX
XX ABR09686;
AC
XX
XX 03-JUL-2003 (first entry)
DT
XX
XX Bacteriophage Qbeta coat protein CP.
DE
XX
XX Bacteriophage Qbeta; coat protein; CP; hypotensive; cerebroprotective;
KM cardiast; nephrotropic; ophthalmological; immunostimulant; vaccine;
KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KM renin-activated angiotensin system; hypertension; stroke; infarction;
KM congestive heart failure; kidney failure; retinal haemorrhage.
XX
XX Bacteriophage Qbeta.
OS
XX
XX WO2003031466-A2.
PN
PD 17-APR-2003.
XX
XX 07-OCT-2002; 2002MO-EP011219.
PF
XX
XX 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-031045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002MO-IB000156.
PR 19-JUL-2002; 2002US-039637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA
XX Bachmann M;
FI WPI; 2003-430264/40.
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
PS Claim 15; Page 92; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide moiety and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune response,
CC including producing antibodies. This is the amino acid sequence of
CC bacteriophage Qbeta coat protein CP used in the preparation of the
CC vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 663; DB 6; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDKQKQTLVNPGRVNPNGVASLSQAGAVALKRKRTVSVSOPSRRK 60
DB 1 AKLEVTTLGNIGKDKQKQTLVNPGRVNPNGVASLSQAGAVALKRKRTVSVSOPSRRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELLAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELLAALLASPL 120

QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 5
ABR44542
ID ABR44542 standard; protein; 132 AA.
XX ABR44542;
AC
XX
XX 23-OCT-2003 (revised)
DT 25-JUL-2003 (first entry)

Bacteriophage Q-beta coat protein SEQ ID NO:10.

XX
XX
XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
KW immunostimulant; cytotoxic; antiallergic; virucide; antibacterial;
KW immune response; immunization; allergy; tumour; breast cancer;
KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Bacteriophage Qbeta.
XX
XX
XX WO2003024481-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 16-SEP-2002; 2002MO-IB004132.
PF
XX
XX 14-SEP-2001; 2001US-0318994P.
PR 22-APR-2002; 2002US-0374145P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (MAURER) MAURER P.
PA (TISST) TISST A.
PA (SCHW) SCHWARZ K.
PA (MEIJ) MEIJERINK E.
PA (LIP) LIPOWSKY G.
PA (PUMP) PUMPHENS P.
PA (CIET) CIETENS I.
PA (RENN) RENHOFFA R.

XX
XX
XX Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G,
PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
XX
XX WPI; 2003-354564/33.
DR

New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
PT viral infections.

XX
XX
XX Disclosure; Page 247; 322pp; English.

XX
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response in an animal. (C) comprises a virus-like particle (VLP), and an
CC immunostimulatory substance. The immunostimulatory substance is bound to
CC the VLP. Also described: (1) enhancing an immune response in an animal by
CC introducing (C) into the animal; (2) producing (C) for enhancing an
CC immune response in an animal; (3) vaccines comprising (C) together with a

CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
CC represent sequences used in the exemplification of the present invention.
CC (updated on 23-OCT-2003 to standardise OS field)

XX
XX
XX SQ Sequence 132 AA;

Query Match 100.0%; Score 663; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDKQKQTLVNPGRVNPNGVASLSQAGAVALKRKRTVSVSOPSRRK 60
DB 1 AKLEVTTLGNIGKDKQKQTLVNPGRVNPNGVASLSQAGAVALKRKRTVSVSOPSRRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELLAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELLAALLASPL 120

QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 6
ADD24117
ID ADD24117 standard; protein; 132 AA.
XX
XX
XX ADD24117;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX
XX Bacteriophage Qbeta coat protein CP.
DE
XX
XX
XX vaccine composition; virus-like particle; core particle;
KW first attachment site; antigen; antigenic determinant; prion protein;
KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
KW prion disease; Bovine Spongiform Encephalopathy; BSE;
KW Creutzfeldt-Jakob Disease; coat protein.

XX
XX
XX Bacteriophage Qbeta.
OS
XX
XX WO2003059386-A2.
PN
XX
XX 24-JUL-2003.
PD
XX
XX 17-JAN-2003; 2003MO-EP000460.
PF
XX
XX 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002MO-IB000166.
PR 08-JUL-2002; 2002US-0393725P.
PR 18-JUL-2002; 2002US-0396590P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA
XX
XX
XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
PI
XX
XX WPI; 2003-598483/56.
DR
XX

PT A vaccine composition for preventing or treating prion diseases (e.g.
PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
PT phage) and at least one prion protein or peptide bound to the virus-like
PT particle.

PS Disclosure; SEQ ID NO 10; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
CC like or a core particle with at least one first attachment site and at
CC least one antigen or antigenic determinant that is a prion protein (PrP)
CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
CC being bound to the virus-like or core particle. The vaccine of the
CC invention may have neuroprotective or anti-inflammatory activity. The
CC composition is useful as a medicament or in manufacturing a medicament
CC for the treatment or prevention of prion diseases. The prion diseases may
CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
CC Disease. The present sequence is the amino acid sequence of a coat
CC protein from a bacteriophage which may be used during the creation of the
CC vaccine composition of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKLEVTLTGNIGKDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60

DB 1 AKLEVTLTGNIGKDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60

OY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVETELAAALLASPL 120

DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVETELAAALLASPL 120

OY 121 LIDAIIDQINPAY 132

DB 121 LIDAIIDQINPAY 132

RESULT 7

ADJ82043
ID ADJ82043 standard; protein; 132 AA.

AC ADJ82043;

DT 06-MAY-2004 (first entry)

XX Protein for RANKL antigen array to treat bone disease.

XX osteopathic; vaccine; core particle; antigenic determinant; RANKL;

KW bone disease; encephalopathy; immune system stimulation.

XX Unidentified.

OS WO2003039225-A2.

XX 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012449.

XX 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-441430/41.

PT New compositions comprising a core particle and at least one antigen or
PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis

PT of bone diseases, particularly mammalian encephalopathies.

PS Disclosure; SEQ ID NO 10; 222pp; English.

XX The invention relates to a composition comprising a core particle having
CC at least one first attachment site, and at least one antigen or antigenic
CC determinant having at least one second attachment site. The antigen or
CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
CC peptide. The second attachment site is (non-) naturally occurring with
CC the antigen or antigenic determinant, and is capable of association with
CC the first attachment site. The antigen or antigenic determinant and the
CC core particle interact through the association to form an ordered and
CC repetitive antigen array. The composition is useful as a medicament, or
CC for the manufacture of a medicament for treating bone diseases. The
CC composition is especially useful for as a vaccine for therapy or
CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
CC and for stimulating mammalian immune system. This sequence represents a
CC protein of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKLEVTLTGNIGKDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60

DB 1 AKLEVTLTGNIGKDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60

OY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVETELAAALLASPL 120

DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVETELAAALLASPL 120

OY 121 LIDAIIDQINPAY 132

DB 121 LIDAIIDQINPAY 132

RESULT 8

ADK17131
ID ADK17131 standard; peptide; 132 AA.

AC ADK17131;

DT 06-MAY-2004 (first entry)

XX Virus-like particle repetitive antigen array peptide #10.

XX antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;

KW interleukin; IL-5; IL-13; eosin; repetitive antigen array;

XX allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

OS WO2003040164-A2.

XX 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012455.

XX 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Jennings G, Sonderegger I;

XX WPI; 2003-441518/41.

PT Composition comprising an ordered and repetitive antigen or antigenic
PT determinant array, useful as a medicament, or for manufacturing a

PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 PT Hodgkin's lymphoma.

XX Disclosure; SEQ ID NO 10; 245bp; English.

XX The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 9.6e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60
 DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 9
 ADJ36300
 ID ADJ36300 standard; protein; 132 AA.

AC ADJ36300;

DT 22-APR-2004 (first entry)

XX Bacteriophage Qbeta coat protein virus-like particle.

XX antiallergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage Qbeta;
 KW coat protein; VLP; adjuvant.

XX Bacteriophage Qbeta.

XX WO2004000351-A1.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-EP006541.

XX 20-JUN-2002; 2002US-0389898P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann MF, Renner WA;

XX WPI; 2004-108361/11.

XX New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with

PT the VLP, useful for enhancing immune response or for treating e.g. tumors
 PT or chronic viral diseases.

XX Example 5; SEQ ID NO 1; 252bp; English.

XX The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
 CC coat protein a virus like particle (VLP) that can be used in the adjuvant
 CC of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;
 Best Local Similarity 100.0%; Pred. No. 9.6e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60
 DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 10
 ADJ67146
 ID ADJ67146 standard; protein; 132 AA.

AC ADJ67146;

DT 06-MAY-2004 (first entry)

XX Bacteriophage Qbeta coat protein for antigen display array.

XX anorectic; core particle; antigenic determinant; ghrelin; P-pill;
 KW antigenic array.

XX Bacteriophage Qbeta.

XX WO2004009124-A2.

XX 29-JAN-2004.

XX 18-JUL-2003; 2003WO-EP007849.

XX 19-JUL-2002; 2002US-0396638P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann MF, Fulurija A;

XX WPI; 2004-132866/13.

XX New composition comprising a core particle having a first attachment site
 PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
 PT peptide having a second attachment site, useful for treating obesity.

XX Claim 12; SEQ ID NO 4; 175bp; English.

XX The invention relates to a new composition comprising: (1) a core
 CC particle with at least one first attachment site; and (1i) at least one
 CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
CC peptide, and where the second attachment site being consisting of an
CC attachment site not naturally occurring with the antigen or antigenic
CC determinant and an attachment site naturally occurring with the antigen
CC or antigenic determinant, where the second attachment site is capable of
CC association to the first attachment site, and where the ghrelin or a
CC ghrelin peptide and the core particle interact through the association to
CC form an ordered and repetitive antigen array. The composition is useful
CC for treating obesity. The repetitive array may form part of a phase or
CC bacterial display array. This peptide corresponds to a Bacteriophage
CC Qbeta coat protein which can used as part of the repetitive or antigenic
CC array.
XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.66-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NYKVOVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFYVTELAALLASPL 120
DB 61 NYKVOVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFYVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 11

ADKS2180
ID ADKS2180 standard; protein; 132 AA.

XX AC ADKS2180;

DT 20-MAY-2004 (first entry)

XX DE Bacteriophage Qbeta coat protein CP.

XX KW neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

XX KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX KW coat protein; CP.

XX OS Bacteriophage Qbeta.

XX PN WO2004016282-A1.

PD 26-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007864.

XX 19-JUL-2002; 2002US-0396639P.

XX 15-MAY-2003; 2003US-0470432P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (NOVS) NOVARTIS PHARMA AG.

XX WPI; 2004-203731/19.

XX Composition comprising a core particle with at least one attachment site,
XX and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
XX such as Alzheimer's disease.

XX Claim 12; SEQ ID NO 4; 184bp; English.

XX The invention describes a novel composition comprising a virus-like core
XX particle with at least one attachment site, and an antigenic amyloid beta

CC 1-6 peptide. The new composition comprises: a core particle with at least
CC one first attachment site; and at least one antigen or antigenic
CC determinant with at least one second attachment site, where the antigen
CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
CC second attachment site comprises: an attachment site not naturally
CC occurring with the antigen or antigenic determinant; or an attachment
CC site naturally occurring with the antigen or antigenic determinant. The
CC second attachment site is capable of association to the first attachment
CC site and the beta 1-6 peptide and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC composition is useful for the manufacture of a medicament for treating
CC Alzheimer's disease and related diseases. This is the amino acid sequence
CC of an RNA bacteriophage coat protein that can be used in the preparation
CC of the compositions and vaccines of the invention.
XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.66-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NYKVOVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFYVTELAALLASPL 120
DB 61 NYKVOVKIOMPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFYVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 12

ABRS6440
ID ABR56440 standard; protein; 328 AA.

XX AC ABR56440;

DT 23-OCT-2003 (revised)

DT 28-JUL-2003 (first entry)

XX DE Bacteriophage Q-beta coat protein SEQ ID NO.11.

XX KW Antigen presenting cell; APC; immune response; virus like particle; VLP;

XX KW cytosolic; virucide; antibacterial; antiparasitic; fungicide;

XX KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

XX KW antihypertoid; antidiabetic; neuroprotective; nootropic; osteopathic;

XX KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;

XX KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;

XX KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;

XX KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;

XX KW inflammatory autoimmune disease.

XX OS Bacteriophage Qbeta.

XX PN WO2003024480-A2.

XX 27-MAR-2003.

XX 16-SEP-2002; 2002WO-1B004252.

XX 14-SEP-2001; 2001US-0318967P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann MF, Storni T, Lechner F;

XX WPI; 2003-363095/34.

XX A composition, useful for enhancing an immune response against an antigen
XX or a virus-like particle, enhancing anti-viral protection in an animal,

PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.

PS Disclosure; Page 168-169; 243pp; English.

XX The present invention describes a composition (C) for enhancing an immune
XX response against an antigen or a virus-like particle in an animal. (C)
XX comprises a virus-like particle (VLP) bound to at least one antigen, or a
XX VLP capable of being recognised by the immune system of the animal. Also
XX described: (1) enhancing an immune response against an antigen or a VLP
XX in an animal comprising introducing (C) into the animal; (2) vaccines
XX comprising (C) together with a pharmaceutical diluent, carrier or
XX excipient; (3) immunising or treating an animal comprising administering
XX the vaccine to the animal, or priming or boosting a T cell response in
XX the animal by administering the vaccine; and (4) enhancing anti-viral
XX protection in an animal comprising introducing (C) into the animal. (C)
XX has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
XX antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
XX antithyroid, antidiabetic, neuroprotective, nocotropic, osteopathic,
XX antirheumatic and antiarthritic activities. (C) or the vaccines can be
XX used for enhancing an immune response against an antigen or a VLP in an
XX animal, enhancing anti-viral protection in an animal, or immunising or
XX treating tumours and infectious diseases such as viral, bacterial,
XX parasitic or fungal infections. The vaccine compositions are also useful
XX for preventing or treating allergies, drug addiction, graft-versus-host
XX disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
XX Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
XX autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
XX represent sequences used in the exemplification of the present invention.
XX (Updated on 23-Oct-2003 to standardise OS field)

SQ Sequence 328 AA;

Query Match 100.0%; Score 663; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.6e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQPSRNNK 60
DB 2 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQPSRNNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALIASPL 121
QY 121 LIDAIDQNLNPAY 132
DB 122 LIDAIDQNLNPAY 133

RESULT 13

ABR44543 standard; protein; 328 AA.

AC ABR44543;

XX 23-OCT-2003 (revised)

DT 25-JUL-2003 (first entry)

XX Bacteriophage Q-beta coat protein SEQ ID NO:11.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
XX hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
XX immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
XX immune response; immunisation; allergy; tumour; breast cancer;
XX neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
XX chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX Bacteriophage Qbeta.

XX WO2003024481-A2.

XX 27-MAR-2003.

XX 16-SEP-2002; 2002WO-IB004132.

XX 14-SEP-2001; 2001US-0318994P.

XX 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (MAUR-) MAURER P.

XX (TISS-) TISSOT A.

XX (SCHW-) SCHWARZ K.

XX (MEIJ-) MEIJERINK E.

XX (LIFO-) LIPOMSKY G.

XX (PUMP-) PUMPENS P.

XX (CIEL-) CIELENS I.

XX (REHN-) REHNOFA R.

XX Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;

XX Pumpens P, Cielens I, Renhofs R, Bachmann MP, Storni T;

XX WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
XX virus-like particles, useful as a vaccine for enhancing an immune
XX response in animals, e.g. for treating or preventing allergies, tumors or
XX viral infections.

XX Disclosure; Page 247-249; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
XX response in an animal. (C) comprises a virus-like particle (VLP), and an
XX immunostimulatory substance. The immunostimulatory substance is bound to
XX the VLP. Also described: (1) enhancing an immune response in an animal by
XX introducing (C) into the animal; (2) producing (C) for enhancing an
XX immune response in an animal; (3) vaccines comprising (C) together with a
XX pharmaceutical diluent, carrier or excipient; and (4) immunising or
XX treating an animal by: (a) administering the vaccine to the animal; (b)
XX priming a T cell response in the animal by administering the vaccine; or
XX (c) boosting a T cell response in the animal by administering the
XX vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
XX antibacterial activities. (1) can be used in vaccines for enhancing an
XX immune response in an animal, particularly a mammal or human.
XX Specifically, (C) is useful for enhancing a B cell response, a T cell
XX response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
XX comprising (C) can also be used for immunising or treating an animal,
XX e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
XX reptiles or fish. (C) is particularly useful in prophylactic or
XX therapeutic vaccines against allergies, tumors (e.g. breast cancers,
XX neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
XX measles or chicken pox), or bacterial infections (e.g. tuberculosis,
XX pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
XX represent sequences used in the exemplification of the present invention.
XX (Updated on 23-Oct-2003 to standardise OS field)

SQ Sequence 328 AA;

Query Match 100.0%; Score 663; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.6e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQPSRNNK 60
DB 2 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQPSRNNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALIASPL 121
QY 121 LIDAIDQNLNPAY 132
DB 122 LIDAIDQNLNPAY 133

RESULT 14

ABG94278
 ID ABG94278 standard; protein; 329 AA.
 AC ABG94278;
 XX
 XX
 DT 06-AUG-2003 (revised)
 DT 10-DEC-2002 (first entry)
 XX
 XX
 DE Bacteriophage Q beta coat protein A1.
 XX
 KM Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KM cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KM vaccine; infectious disease.
 XX
 XX
 OS Bacteriophage.
 XX
 PN WO200256905-A2.
 PD
 PD 25-JUL-2002.
 PF
 PF 21-JAN-2002; 2002MO-1B000166.
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 P1 Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
 P1 Piossek C;
 XX
 DR WPI: 2002-627351/67.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 PS
 PS Claim 7; Page 416-417; 441pp; English.
 CC
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytotoxic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 06
 CC -AUG-2003 to correct OS field.)
 CC
 SQ Sequence 329 AA;

Query Match 100.0%; Score 663; DB 5; Length 329;
 Beet Local Similarity 100.0%; Pred. No. 3,6e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
 |||

DB 2 AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 61
 QY 61 NKYGVOKIOMPACTANGSCDPSVTRQAYADVTFSFTQSTDEERAFVTEIAALLASPL 120
 DB 62 NKYGVOKIOMPACTANGSCDPSVTRQAYADVTFSFTQSTDEERAFVTEIAALLASPL 121
 QY 121 LIDAIDQINPAY 132
 DB 122 LIDAIDQINPAY 133
 RESULT 15
 ABG80590
 ID ABG80590 standard; protein; 329 AA.
 AC ABG80590;
 XX
 XX
 DT 29-AUG-2003 (revised)
 DT 29-NOV-2002 (first entry)
 XX
 XX
 DE Bacteriophage Q-beta A1 protein.
 XX
 KM Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; Igg-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.
 XX
 OS Bacteriophage Qbeta.
 XX
 PN WO200256907-A2.
 PD
 PD 25-JUL-2002.
 PF
 PF 21-JAN-2002; 2002MO-1B000166.
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAURER) MAURER P.
 PA (LECHNER) LECHNER F.
 PA (ORTMANN) ORTMANN R.
 PA (LUDEND) LUDEND R.
 PA (STAV) STAUENBIEL M.
 PA (FREY) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Luedend R, Stauenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 DR WPI: 2002-636514/68.
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 PS
 PS Disclosure; Page 393-394; 418pp; English.
 CC
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is

CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IGF-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The antigens are modified to possess
CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
CC virus like particle or bacterial protein (the scaffold protein). The
CC present sequence is bacterial protein or peptide which is coupled to the
CC modified antigen to form the molecular antigen array. (Updated on 29-AUG-
CC 2003 to standardise OS field)

XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 663; DB 5; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.6e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AKLETTIGNIGKDGKQTLVLRGVPPTNGVASTLSQAGVPALEKRVTVSVQPSRNK	60
DB	2	AKLETVTLGNIGKQTLVLRGVPPTNGVASTLSQAGVPALEKRVTVSVQPSRNK	61
QY	61	NYKVQKIQNPFTACTANGSCDPSVTRQAVADVTFSTQYSTDERAAFVTELAALLASPL	120
DB	62	NYKVQKIQNPFTACTANGSCDPSVTRQAVADVTFSTQYSTDERAAFVTELAALLASPL	121
QY	121	LIDAIQDLNPAY	132
DB	122	LIDAIQDLNPAY	133

Search completed: January 4, 2005, 09:10:58
Job time : 41.6824 secs


```

? FILE REFERENCE: 100564-00079
? CURRENT APPLICATION NUMBER: US/09/948,722
? CURRENT FILING DATE: 2002-04-08
? PRIOR APPLICATION NUMBER: US 09/485,717
? PRIOR FILING DATE: 2000-02-22
? PRIOR APPLICATION NUMBER: PCT/EP98/05109
? PRIOR FILING DATE: 1998-06-12
? PRIOR APPLICATION NUMBER: EP 97/114,614.7
? PRIOR FILING DATE: 1997-08-23
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 2
? LENGTH: 626
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
? OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
? OTHER INFORMATION: escape domain
? US-09-948-722-2

```

Query Match	13.5%;	Score 89.5;	DB 4;	Length 626;
Best Local Similarity	23.5%;	Pred. No. 0.027;		
Matches	31;	Conservative	23;	Mismatches 43; Indels 35; Gaps 5;
Qy	13	KDKGKQTVL-----NPRGVNPTNGVASTLSQAGA-----	VPALERLV	48
		:::	:::	:
Db	138	KDGNREYIVVEKKKSSINONNADIQVNAISSLTYPGALVYKANSELVENQPDVLPIPKRRSL		197
Qy	49	TVSVQSPSRNNKYNKVOYKIONPFIACIATNGSCDPSVTR-----	QAYADVTFPSFTQYSTD	102
		:: :: :: ::	::	
Db	198	TLISIDLGMTQDNKIIVK--NATKSNVNAVNTLVERMNEKYAQAYPNVS---AKIDYD		252
		:: :: ::		
Qy	103	EEPAFVETLEAA	114	
		:: :::		
Db	253	DEMAYESQOLIA	264	
		:: :::		

```

RESULT 3
US-09-328-352-4249.
; Sequence 4249, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4249
; LENGTH: 409
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

```

Query Match 11.5%; Score 76.5; DB 4; Length 409;
Best Local Similarity 25.8%; Pred. No. 0.64;
Matches 34; Conservative 20; Mismatches 53; Indels 25; Gaps 6;

```

QY      7 TLGNICRDKQKQTLVLN---PR-----GVNPTNGVASLSQAGAVPALEKRYTV-SVSPQS 56
Db      109 SLINFTKDYRGGGTRILNVNVRNALISFANVPDGGTTP-----IAKPNQORLITIDLLAPG 163
QY      57 RNRKNVYVYKIQNPACTANGSCDPSVYRQAYADVTFESFYQYSNDERAFVRETELALL 116
Db      164 RTGGSN---AIAYLIREGFTNNALVPENTAKYSEITP-----EEVMESVKTIAHMLK 213
QY      117 ASPLLDIDAI DQL 128
Db      214 ASKQILIDDLPEQL 225

```

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RESULT 4
US-09-206-942-49
; Sequence 49, Application US/09206942
; Patent No. 643269
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; TITLE OF INVENTION: Molecular Weight Proteins
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; US-09-206-942-49

```

	Query Match	11.2%	Score 74;	DB 4;	Length 1073;	
	Best Local Similarity	22.8%;	Pred. No. 6.2;	Mismatches 51;	Indels 18;	Gaps 4;
	Matches	28;	Conservative	26;		
Qy	4	EVTLLGNIGDKGKOTLVLPNG-----VNPFGVASISQAQAVPALEKRVTVSYSQ	54			
	:	: :: :	:	:: :	:	:: :
Dd	766	KTLTVGVN--SGNVITVYTAIRGMLTTLAGSTINTNTSVTSSGGELGEVTKATVSITA	823			
	:	:: ::	:	:	:	:
Qy	55	PSRN---KNRYKOVKIQNPACTANGSCDPSVTRQAYADYTFSEFTQYSTDEERAFATE	111			
	:	: :: :	:	:: :	:	:: :
Dd	824	TAGSLFVKGAKINATEGTALTLLASSG----KLTFEASNTTSKAGVDLSAODGISIAGQ	879			
	:	:: ::	:	:	:	:
Qy	112	LAA 114				
	:	::	:	:	:	:
Dd	880	ISA 882				
	:	::	:	:	:	:

```

RESULT 5
US-09-206-942-47
Sequence 47, Application US/09206942
Patent No. 6432659
GENERAL INFORMATION:
APPLICANT: Loommore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 MI:jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 47
;
; LENGTH: 1079
;
; TYPE: PRN
;
; ORGANISM: Haemophilus influenzae
;
US-09-206-942-47

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Query Match	11.2%;	Score 74;	DB 4;	Length 1079;
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Matches 28; Conservative 26; Mismatches 51; Indels 18; Gaps 4;

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QY      4 EYVTLGNIGKOKQTLVLPNG-----VNPINGASLSQAGVPALEKRTVTSVQ 54
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      772 KILTVGNV--SGNTVTVANRGALTTLTAGSTINGNGVTSOSGEGIGEVTKTSVTA 829
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      55 PSNN--RKNKYVQYKIQNPACTIANGSCDSVTRQAVDYTFEFTQYSTIDEEAPRTE 1111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

DB 830 TAGSLTVKGAKNINTEGRATITASSG---KLTTEASSNITSAGQVDSIAQDSIAGQ 885
QY 112 LAA 114
DB 886 ISA 888

RESULT 6

US-09-045-186-2
; Sequence 2, Application US/09045186
; Patent No. 6087154

GENERAL INFORMATION:

APPLICANT: Baez, Melvyn
APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-045-186-2

Query Match 11.1%; Score 73.5; DB 3; Length 383;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGVPALEKRVTVSVSOPSRNKNYKVQVK 67
DB 138 RHQLINFRGWRPNRHHAYGVIAVWLVAVASSLPLIYQ--VMDEPRQN----- 186
QY 68 IONPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFAVTELAAL 115
DB 187 -----VTLDAYKDKVVCDFPDSHRLSYTLLLVL 218

RESULT 7

US-08-232-144-4
; Sequence 4, Application US/08232144
; Patent No. 5571695

GENERAL INFORMATION:

APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
APPLICANT: SHINE, John
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F199, Ernst & Kurz
STREET: 555 13th St, N.W., Suite 701-East

CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,144
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-144-4

Query Match 11.1%; Score 73.5; DB 1; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4; Indels 35; Gaps 4;
Matches 28; Conservative 12; Mismatches 33;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGVPALEKRVTVSVSOPSRNKNYKVQVK 67
DB 138 RHQLINFRGWRPNRHHAYGVIAVWLVAVASSLPLIYQ--VMDEPRQN----- 186
QY 68 IONPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFAVTELAAL 115
DB 187 -----VTLDAYKDKVVCDFPDSHRLSYTLLLVL 218

RESULT 8
US-08-555-268A-15
; Sequence 15, Application US/08555268A
; Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinschenk, Richard J.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,268A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

```

REFERENCE/DOCKET NUMBER: 44743-Z/JPM/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-555-268A-15

Query Match      11.1%; Score 73.5; DB 2; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4.

Oy      16 KQTLVLRGCVNPTN-----GVA--SSQAGAVALEKKRYTVSVSQQSRKRAKYQVK 67
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      138 RHQLINRGKRPNNRHAYVGIATVWIAVASSLPFLYQ--VMDEPFQN----- 186

Oy      68 IQNPCTANGSCDPSYTRQAYADVTFSFTQYSTDEERAFVTEIAAL 115
       || || || || || || || || || || || || || || || || || || || ||
Db      187 -----VTLDAIKDKYVCFDPQPPSDSHSLSTLTLLVL 218

RESULT 9
US-09-200-673-15
Sequence 15, Application US/09200673A
Patent No. 6316203
GENERAL INFORMATION:
APPLICANT: Weinschank, Christophe P. G.
APPLICANT: Weinschank, Richard L.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
TITLE OF INVENTION: in Such Methods, and DNA Encoding A Hypothalamic
TITLE OF INVENTION: Acyclical Neuropeptide Y/Peptide Y Receptor (Y5)
FILE REFERENCE: 46166-B2/JPM
CURRENT APPLICATION NUMBER: US/09/200,673A
CURRENT FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: 08/566,096
EARLIER FILING DATE: 1995-12-01
EARLIER APPLICATION NUMBER: 08/349,025
EARLIER FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-09-200-673-15

Query Match      11.1%; Score 73.5; DB 3; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4.

Oy      16 KQTLVLRGCVNPTN-----GVA--SSQAGAVALEKKRYTVSVSQQSRKRAKYQVK 67
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      138 RHQLINRGKRPNNRHAYVGIATVWIAVASSLPFLYQ--VMDEPFQN----- 186

Oy      68 IQNPCTANGSCDPSYTRQAYADVTFSFTQYSTDEERAFVTEIAAL 115
       || || || || || || || || || || || || || || || || || || || ||
Db      187 -----VTLDAIKDKYVCFDPQPPSDSHSLSTLTLLVL 218

RESULT 10
US-10-013-846-4
Sequence 4, Application US/10013846
Patent No. 6566367
GENERAL INFORMATION:
APPLICANT: Baktavatchalam, Rajagopal
APPLICANT: Blum, Charles A

```

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APPLICANT: Brietmann, Harry L
APPLICANT: Darrow, James W
APPLICANT: De Lombaert, Stephane
APPLICANT: Hutchison, Alan
APPLICANT: Tian, Jennifer
APPLICANT: Zheng, Xiaozhang
APPLICANT: Elliott, Richard L
APPLICANT: Hammond, Maryls
TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
TITLE OF INVENTION: 3H-epitroisobenzofuran-1,4'-piperidines
FILE REFERENCE: N00.2001
CURRENT APPLICATION NUMBER: US/10/013.846
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,990
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 384
TYPE: PRT
ORGANISM: homosapiens
US-10-013-846-4

Query Match 11.1%; Score 73.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No.1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

OY 16 KQTLVNPGRVNPNT-----GVA---SISQAGAVPALEKRYTVSVSQPSRNRKMYQYVK 67
Dh 138 RHQLIINPGRMPNNRHHAYVGLAIYWLAVASSLPILYQ--VWTDDEFQK----- 186
OY 68 IQNPFCTANGSCDPSYTRQAYADVTFSFTQYSTDERAPFRTLAAL 115
Dh 187 -----VTLDAKYKDYVCFPDQPSDSHRLSYTLLLVL 218

RESULT 11
US-09-708-392-9
Sequence 9, Application US/09708392
Patent No. 6734186
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Maw, G
TITLE OF INVENTION: Pharmaceutical
FILE REFERENCE: PC10343AKM
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: GB 9926437.6
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 0004021.2
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 0016563.9
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: GB 0017741.3
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 60/221,014
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/221,093
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 384

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TYPE: PRT
ORGANISM: Homo sapiens
US-09-708-392-9

Query Match 11.1%; Score 73.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGAVPALERKVTYVSQPSRNKRYKVQK 67
DB 138 RHQLINPRGMRPNRHAYGVIAVIMVLAVASSLPFLIQ--VMTDEPFQN----- 186
QY 68 IONPACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKVCDFDPSPDSHRLSYTTLVLVL 218

RESULT 12

PCT-US93-05039-3
Sequence 3, Application PC/TUS9305039
GENERAL INFORMATION:
APPLICANT: Claes R. Wahlestedt
TITLE OF INVENTION: Human Neuropeptide Y/Peptide YY
TITLE OF INVENTION: Receptor of the Y1-Type and
TITLE OF INVENTION: Antisense Oligonucleotides
TITLE OF INVENTION: Thereto Which Inhibit Vasoconstriction
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05039
FILING DATE: 19930527
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1250
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-05039-3

Query Match 11.1%; Score 73.5; DB 5; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGAVPALERKVTYVSQPSRNKRYKVQK 67
DB 138 RHQLINPRGMRPNRHAYGVIAVIMVLAVASSLPFLIQ--VMTDEPFQN----- 186
QY 68 IONPACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKVCDFDPSPDSHRLSYTTLVLVL 218

RESULT 13

US-08-817-869-3
Sequence 3, Application US/08817869
Patent No. 6001970
GENERAL INFORMATION:

APPLICANT: STRADER, CATHERINE D.
APPLICANT: CASCIERI, MARGARET A.
APPLICANT: MACNEIL, DOUGLAS J.
TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM H. NICHOLSON
STREET: 126 EAST LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,017
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: NICHOLSON, WILLIAM H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 19339Y PCT
TELEPHONE: (732) 594-1348
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-869-3

Query Match 11.1%; Score 73.5; DB 3; Length 411;
Best Local Similarity 25.9%; Pred. No. 1.6;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGAVPALERKVTYVSQPSRNKRYKVQK 67
DB 141 RHQLINPRGMRPNRHAYGVIAVIMVLAVASSLPFLIQ--VMTDEPFQN----- 189
QY 68 IONPACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVTELAAL 115
DB 190 -----VTLDAYKDKVCDFDPSPDSHRLSYTTLVLVL 221

RESULT 14

PCT-US93-14377-3
Sequence 3, Application PC/TUS9314377
GENERAL INFORMATION:
APPLICANT: STRADER, CATHERINE D.
APPLICANT: CASCIERI, MARGARET A.
APPLICANT: MACNEIL, DOUGLAS J.
TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APOLLINIA
STREET: 126 EAST LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14377
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,017
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: APPOULINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19339Y PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-14377-3

Query Match 11.1%; Score 73.5; DB 5; Length 411;
Best Local Similarity 25.9%; Pred. No. 1.6;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVNPBGVNPVN-----GVA---SLSQAGVPALEKRVTVSVQPSNRKRYVQVK 67
DB 141 RHQLIINPRGMRRHAYVGIWVLAVASSLPILYQ--VWDEPFQN----- 189
190 -----VTLDAYKDYKVCYCFQPPSDSHRLSYTLLVL 221

RESULT 15
US-08-397-411-13
Sequence 13, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: B-specific Antibody Effective to Treat
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-13

Query Match 10.8%; Score 71.5; DB 3; Length 279;
Best Local Similarity 24.0%; Pred. No. 1.5;
Matches 23; Conservative 19; Mismatches 37; Indels 17; Gaps 3;

QY 29 TNGVASLSQAGVPALEKRVTVSVQPSNRKRYVQVKQNPACTANGSCDP----- 82
DB 179 SSGGLVSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVE-PKSCDKTHTCPCPCPAG 237
QY 83 --SVTRQAVDYTFSTFGYSTDEERAFVTELAAL 116
DB 238 GLTDTLQAFD-----QLEDKKSALOTETIANML 265

Search completed: January 4, 2005, 09:35:40
Job time : 11.3622 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignment)
1450.557 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663 AKLETVTLGNIGKDKQTLV.....ALLASPLLDALDQINPAY 132

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	663	100.0	132	Sequence 10, Appl
3	663	100.0	132	Sequence 10, Appl
4	663	100.0	132	Sequence 159, App
5	663	100.0	132	Sequence 159, App
6	663	100.0	132	Sequence 10, Appl
7	663	100.0	132	Sequence 10, Appl
8	663	100.0	132	Sequence 10, Appl
9	663	100.0	132	Sequence 4, Appl
10	663	100.0	132	Sequence 4, Appl
11	663	100.0	132	Sequence 11, Appl
12	663	100.0	328	Sequence 11, Appl
13	663	100.0	328	Sequence 11, Appl

14	663	100.0	329	US-10-289-454-11	Sequence 11, Appl
15	663	100.0	329	US-10-050-902-217	Sequence 217, App
16	663	100.0	329	US-10-050-898-217	Sequence 217, App
17	663	100.0	329	US-10-346-190-11	Sequence 11, Appl
18	663	100.0	329	US-10-465-811-2	Sequence 2, Appl
19	663	100.0	329	US-10-289-456-11	Sequence 11, Appl
20	663	100.0	329	US-10-622-064-4	Sequence 4, Appl
21	663	100.0	329	US-10-622-124-5	Sequence 5, Appl
22	663	100.0	329	US-10-622-087-5	Sequence 5, Appl
23	663	98.8	132	US-10-243-739-23	Sequence 23, Appl
24	663	98.8	132	US-10-243-739-26	Sequence 26, Appl
25	663	98.8	132	US-10-244-065-23	Sequence 26, Appl
26	663	98.8	132	US-10-244-065-26	Sequence 26, Appl
27	663	98.8	132	US-10-289-454-23	Sequence 23, Appl
28	663	98.8	132	US-10-289-454-26	Sequence 25, App
29	663	98.8	132	US-10-050-902-255	Sequence 25, App
30	663	98.8	132	US-10-050-902-259	Sequence 25, App
31	663	98.8	132	US-10-050-898-255	Sequence 25, App
32	663	98.8	132	US-10-050-898-259	Sequence 25, App
33	663	98.8	132	US-10-346-190-23	Sequence 23, Appl
34	663	98.8	132	US-10-346-190-26	Sequence 26, Appl
35	663	98.8	132	US-10-465-811-14	Sequence 14, Appl
36	663	98.8	132	US-10-465-811-17	Sequence 17, Appl
37	663	98.8	132	US-10-289-456-23	Sequence 23, Appl
38	663	98.8	132	US-10-289-456-26	Sequence 26, Appl
39	663	98.8	132	US-10-622-064-6	Sequence 6, Appl
40	663	98.8	132	US-10-622-064-9	Sequence 9, Appl
41	663	98.8	132	US-10-622-124-17	Sequence 17, Appl
42	663	98.8	132	US-10-622-124-20	Sequence 20, Appl
43	663	98.8	132	US-10-622-087-17	Sequence 17, Appl
44	663	98.8	132	US-10-622-087-20	Sequence 20, Appl
45	663	98.3	132	US-10-243-739-24	Sequence 24, Appl

ALIGNMENTS

US-10-243-739-10		RESULT 1
Sequence 10, Application US/10243739		
Publication No. US20030091593A1		
GENERAL INFORMATION:		
APPLICANT: Bachmann, Martin F.		
APPLICANT: Stornli, Tazio		
APPLICANT: Lechner, Franziska		
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of		
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles		
FILE REFERENCE: 1700.0210001		
CURRENT APPLICATION NUMBER: US/10/243,739		
CURRENT FILING DATE: 2002-09-16		
PRIOR APPLICATION NUMBER: 60/318,967		
PRIOR FILING DATE: 2001-09-14		
NUMBER OF SEQ ID NOS: 73		
SOFTWARE: PatentIn version 3.1		
SEQ ID NO 10		
LENGTH: 132		
TYPE: PRT		
ORGANISM: Bacteriophage Q-beta		
US-10-243-739-10		
Query Match	100.0%; Score 663; DB 14;	Length 132;
Best Local Similarity	100.0%; Pred. No. 1.6e-66;	
Matches 132; Conservative 0; Mismatches 0;		Indels 0; Gaps 0;
QY	1 AKLETVTLGNIGKDKQTLVLPNGVPTNGASISQGAVALKRYTVSVSOSRNNK 60	
DB	1 AKLETVTLGNIGKDKQTLVLPNGVPTNGASISQGAVALKRYTVSVSOSRNNK 60	
QY	61 NKVVQVKTQNPACTANGSCDPSVTROAVADYTFSTQYSTDEBAFVYTELAALASPL 120	
DB	61 NKVVQVKTQNPACTANGSCDPSVTROAVADYTFSTQYSTDEBAFVYTELAALASPL 120	
QY	121 LIDAIDQINPAY 132	

Db 121 LIDAIQOLNPAY 132

RESULT 2

US-10-244-065-10
; Sequence 10, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tisot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerald
; APPLICANT: Bumpens, Paul
; APPLICANT: Clelens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Partic
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-10

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNKK 60
DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNKK 60
QY 61 NKVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NKVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 3

US-10-289-454-10
; Sequence 10, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jenning, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-289-454-10

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNKK 60
DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNKK 60
QY 61 NKVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NKVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 4

US-10-050-902-159
; Sequence 159, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q Beta
US-10-050-902-159

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNKK 60
DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNKK 60
QY 61 NKVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NKVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 5
US-10-050-898-159
; Sequence 159, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisbet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufendiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q Beta
US-10-050-898-159

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTYSTDEERAFVTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 6
US-10-346-190-10
; Sequence 10, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pellioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-346-190-10

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTYSTDEERAFVTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 7
US-10-465-811-1
; Sequence 1, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN P
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-465-811-1

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTYSTDEERAFVTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 8
US-10-289-456-10
; Sequence 10, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:

APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
CURRENT FILING DATE: 2002-11-07
PRIORITY APPLICATION NUMBER: PCT/IB02/00166
PRIORITY FILING DATE: 2002-01-21
PRIORITY APPLICATION NUMBER: US 10/050,902
PRIORITY FILING DATE: 2002-01-18
PRIORITY APPLICATION NUMBER: US 60/396,635
PRIORITY FILING DATE: 2002-07-19
PRIORITY APPLICATION NUMBER: US 60/331,045
PRIORITY FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-289-456-10

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRK 60
DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRK 60
QY 61 NYKQVQKIONPRACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
DB 61 NYKQVQKIONPRACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 LIDAIQDQNPAY 132

RESULT 9
US-10-622-064-3
Sequence 3, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
CURRENT FILING DATE: 2003-07-18
PRIORITY APPLICATION NUMBER: US 60/396,575
PRIORITY FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-064-3

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRK 60
DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRK 60
QY 61 NYKQVQKIONPRACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
DB 61 NYKQVQKIONPRACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120

QY 121 LIDAIQDQNPAY 132
DB 121 LIDAIQDQNPAY 132

RESULT 10
US-10-622-124-4
Sequence 4, Application US/10622124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurja, Alma
TITLE OF INVENTION: Gritelin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
CURRENT FILING DATE: 2003-07-18
PRIORITY APPLICATION NUMBER: US 60/396,638
PRIORITY FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-124-4

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRK 60
DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRK 60
QY 61 NYKQVQKIONPRACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
DB 61 NYKQVQKIONPRACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 LIDAIQDQNPAY 132

RESULT 11
US-10-622-087-4
Sequence 4, Application US/10622087
Publication No. US20040141984A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tibbott, Alain
APPLICANT: Ortman, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Staufenbiel, Matthias
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIORITY APPLICATION NUMBER: US 60/396,639
PRIORITY FILING DATE: 2002-07-19
PRIORITY APPLICATION NUMBER: US 60/470,432
PRIORITY FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-087-4

Query Match 100.0%; Score 663; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
Db 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 120
Db 61 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 12
US-10-243-739-11
; Sequence 11, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-11

Query Match 100.0%; Score 663; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
Db 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 61
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 120
Db 62 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 121
Qy 121 LIDAIQOLNPAY 132
Db 122 LIDAIQOLNPAY 133

RESULT 13
US-10-244-065-11
; Sequence 11, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurel, Patrick
; APPLICANT: Tisseot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meljersink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; TITLE OF INVENTION: Method of Preparation and Use
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-11

Query Match 100.0%; Score 663; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
Db 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 61
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 120
Db 62 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 121
Qy 121 LIDAIQOLNPAY 132
Db 122 LIDAIQOLNPAY 133

RESULT 14
US-10-289-454-11
; Sequence 11, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta CP
US-10-289-454-11

Query Match 100.0%; Score 663; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
Db 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 61
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 120
Db 62 NYKVQVKIQNPACTCANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELAALLASPL 121
Qy 121 LIDAIQOLNPAY 132
Db 122 LIDAIQOLNPAY 133
```

RESULT 15
US-10-050-902-217

/ Sequence 217, Application US/10050902
/ Publication No. US20030175290A1

/ GENERAL INFORMATION:

/ APPLICANT: Renner, Wolfgang A.

/ APPLICANT: Bachmann, Martin

/ APPLICANT: Tisot, Alain

/ APPLICANT: Maurer, Patrick

/ APPLICANT: Lechner, Franziska

/ APPLICANT: Seibel, Peter

/ APPLICANT: Blosek, Christine

/ TITLE OF INVENTION: Molecular Antigen Array

/ FILE REFERENCE: 1700.0190004

/ CURRENT FILING DATE: 2002-01-18

/ PRIOR FILING DATE: 2001-01-19

/ PRIOR FILING DATE: 2001-05-04

/ PRIOR FILING DATE: 2001-10-05

/ PRIOR FILING DATE: 2001-11-07

/ NUMBER OF SEQ ID NOS: 350

/ SOFTWARE: Patent Ver. 2.1

/ SEQ ID NO 217

/ LENGTH: 329

/ TYPE: PRT

/ ORGANISM: Bacteriophage Q-beta

US-10-050-902-217

Query Match 100.0%; Score 663; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AKLETVLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALKEKRVTVSVSQPSRNRK	60
DB	2	AKLETVLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALKEKRVTVSVSQPSRNRK	61
QY	61	NYKVQVKTQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVRTETLALLASPL	120
DB	62	NYKVQVKTQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVRTETLALLASPL	121
QY	121	LIDAIQQLNPAY	132
DB	122	LIDAIQQLNPAY	133

Search completed: January 4, 2005, 09:41:20
Job time : 33.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTVLGNIGKDGRTLV.....ALLASPLIDAIQQLNPAV 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	5	ABG94319
2	664	100.0	132	5	ABG80631
3	664	100.0	132	6	ABR56456
4	664	100.0	132	6	ABU09692
5	664	100.0	132	6	ABR44559
6	664	100.0	132	7	ADD24134
7	664	100.0	132	7	ADJ82060
8	664	100.0	132	7	ADK17148
9	664	100.0	132	8	ADJ36317
10	664	100.0	132	8	ADJ67163
11	664	100.0	132	8	ADK52197
12	661	99.5	132	5	ABG94320
13	661	99.5	132	5	ABG80632
14	661	99.5	132	6	ABR56455
15	661	99.5	132	6	ABU09693
16	661	99.5	132	6	ABR44558
17	661	99.5	132	7	ADD24133
18	661	99.5	132	7	ADJ82059
19	661	99.5	132	7	ADK17147
20	661	99.5	132	8	ADJ36316
21	661	99.5	132	8	ADJ67162
22	661	99.5	132	8	ADK52196
23	658	99.1	132	5	ABG94318
24	658	99.1	132	5	ABG80630
25	658	99.1	132	6	ABR56454

26	658	99.1	132	6	ABU09691
27	658	99.1	132	6	ABR44557
28	658	99.1	132	7	ADD24132
29	658	99.1	132	7	ADJ82058
30	658	99.1	132	7	ADK17146
31	658	99.1	132	8	ADJ36315
32	658	99.1	132	8	ADJ67161
33	658	99.1	132	8	ADK52195
34	655	98.6	132	5	ABG94316
35	655	98.6	132	5	ABG80628
36	655	98.6	132	6	ABR56452
37	655	98.6	132	6	ABU09689
38	655	98.6	132	6	ABR44555
39	655	98.6	132	7	ADD24130
40	655	98.6	132	7	ADJ82056
41	655	98.6	132	7	ADK17144
42	655	98.6	132	8	ADJ36313
43	655	98.6	132	8	ADJ67159
44	655	98.6	132	8	ADK52193
45	652	98.2	132	5	ABG94233

ALIGNMENTS

RESULT 1	ABG94319	standard; protein; 132 AA.
ID	ABG94319	
XX	ABG94319;	
AC		
XX		
DT	29-AUG-2003 (revised)	
DT	10-DEC-2002 (first entry)	
XX		
DE	PQB259 protein.	
XX		
KW	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;	
KW	cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;	
KW	vaccine; infectious disease.	
XX		
OS	unidentified bacteriophage.	
XX		
PN	WO200256905-A2.	
PD		
XX	25-JUL-2002.	
XX		
PF	21-JAN-2002; 2002MO-IB000166.	
XX		
PR	19-JAN-2001; 2001US-0262379P.	
PR	04-MAY-2001; 2001US-0286549P.	
PR	05-OCT-2001; 2001US-0326998P.	
PR	07-NOV-2001; 2001US-0331045P.	
XX		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
PI		
XX	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Seibel P;	
PI	Piossek C;	
XX	WPI; 2002-627351/67.	
DR		
XX		
XX		
PT	Molecular antigen array used in the production of vaccines for infectious diseases.	
PT		
PS	Claim 18; Page 146; 441pp; English.	
XX		
CC	This invention relates to a novel ordered and repetitive antigen array	
CC	used in the production of vaccines for infectious diseases. The invention	
CC	also discloses a composition comprising a non-natural molecular scaffold	
CC	comprising a core particle selected from a core particle of a non-natural	
CC	origin and a core particle of natural origin and an organiser comprising	
CC	at least one first attachment site, where the organiser is connected to	
CC	the core particle by at least one covalent bond. Also disclosed is an	
CC	antigen or antigenic determinant with at least one second attachment	

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, anti-allergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 DB 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 QY 61 NKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
 DB 61 NKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 2
 ABG80631
 ID ABG80631 standard; protein; 132 AA.

XX ABG80631;

XX 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-251.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.
 OS Synthetic.

PN WO200256907-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002MO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326988P.
 PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEB/) LUEBEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 PI Maurer P., Lechner F., Ortmann R., Luebend R., Staufenbiel M., Frey P;
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Piossek C;
 XX WPI, 2002-636514/68.

DR Molecular antigen array used in the production of vaccines for infectious
 XX diseases.

PS Example 18; Page 403; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 DB 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 QY 61 NKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
 DB 61 NKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 3
 ABR56456
 ID ABR56456 standard; protein; 132 AA.

XX ABR56456;
AC
XX 28-JUN-2003 (first entry)
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:27.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KM cytosolic; virucide; antibacterial; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
KM antithyroid; antidiabetic; neuroprotective; nocotropic; osteopathic;
KM antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.
XX Bacteriophage Qbeta.
OS Synthetic.
XX
XX WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
XX PF
XX 14-SEP-2001; 2001US-0318967P.
XX PR
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA
XX Bachmann M, Storni T, Lechner F;
PI
XX WPI, 2003-363095/34.
XX DR
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 183; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
CC antithyroid, antidiabetic, neuroprotective, nocotropic, osteopathic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ARLEVTTLGNIGKGRQTLVLNPRGVNPTNGVASLSQAGAVPALKEKRVTSVSQPSRRNK 60

DB 1 ARLEVTTLGNIGKGRQTLVLNPRGVNPTNGVASLSQAGAVPALKEKRVTSVSQPSRRNK 60
QY 61 NYKVQVKIQLNPACTANGSCDPSVTROKXADVTSGFTQYSTDEERAFRTETLAALLASPL 120
DB 61 NYKVQVKIQLNPACTANGSCDPSVTROKXADVTSGFTQYSTDEERAFRTETLAALLASPL 120
QY 121 LIDAIQQLNPAY 132
DB 121 LIDAIQQLNPAY 132
RESULT 4
ABU09692
ID ABU09692 standard; protein; 132 AA.
XX
XX ABU09692;
AC
XX
XX 03-JUN-2003 (first entry)
XX
XX Bacteriophage Qbeta mutant coat protein #4.
XX
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
KM cardiast; nephrotropic; opthalmological; immunostimulant; vaccine;
KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KM renin-activated angiotensin system; hypertension; stroke; infarction;
KM congestive heart failure; kidney failure; retinal haemorrhage; mutant;
KM mutin.
XX
XX Bacteriophage Qbeta.
OS
XX WO2003031466-A2.
XX PN
XX 17-APR-2003.
XX PD
XX 07-OCT-2002; 2002WO-EP011219.
XX PF
XX 05-OCT-2001; 2001US-0326998P.
XX PR 07-NOV-2001; 2001US-0331045P.
XX PR 18-JAN-2002; 2002US-00050902.
XX PR 21-JAN-2002; 2002WO-IB000166.
XX PR 19-JUN-2002; 2002US-0396637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA
XX Bachmann M;
PI
XX WPI, 2003-430264/40.
XX DR
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
XX Claim 20; Page 94; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage Qbeta coat protein used in the preparation of the
CC vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEETVLTGNTGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
 DB 1 ALEETVLTGNTGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60

QY 61 NKVVQVKIQNPACTRANGSCDPSVTRQKADVTFFSTQYSTDEERAFVTEIAALLASPL 120
 DB 61 NKVVQVKIQNPACTRANGSCDPSVTRQKADVTFFSTQYSTDEERAFVTEIAALLASPL 120

QY 121 LIDAIDQLNPAV 132
 DB 121 LIDAIDQLNPAV 132

RESULT 5
 ABR44559
 ID ABR44559 standard; protein; 132 AA.
 AC ABR44559;
 DT 25-JUL-2003 (first entry)
 XX

DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:27.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytotoxic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Bacteriophage Qbeta.
 OS Synthetic.
 PN WO2003024481-A2.

PD 27-MAR-2003.
 XX

PF 16-SEP-2002; 2002WO-IB004132.
 XX

PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER) MAURER P.
 PA (TISSOT) TISSOT A.
 PA (SCHWAB) SCHWAB K.
 PA (MEIJER) MEIJERINK E.
 PA (LIPO) LIPOWSKY G.
 PA (PUMP) PUMPENS P.
 PA (CIELE) CIELENS I.
 PA (RENNHOF) RENNHOF R.

PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cieles I, Renhof R, Bachmann M, Storni T;
 DR WPI: 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX

XX Disclosure; Page 262; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing an immune response in an
 CC animal; (3) vaccines comprising (C) for enhancing an
 CC immune response in an animal; (4) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC printing a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytotoxic, antiallergic, virucide and
 CC antibacterial activities. (I) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumors (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 CC

SEQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEETVLTGNTGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
 DB 1 ALEETVLTGNTGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60

QY 61 NKVVQVKIQNPACTRANGSCDPSVTRQKADVTFFSTQYSTDEERAFVTEIAALLASPL 120
 DB 61 NKVVQVKIQNPACTRANGSCDPSVTRQKADVTFFSTQYSTDEERAFVTEIAALLASPL 120

QY 121 LIDAIDQLNPAV 132
 DB 121 LIDAIDQLNPAV 132

RESULT 6
 ADD24134
 ID ADD24134 standard; protein; 132 AA.
 AC ADD24134;
 DT 15-JAN-2004 (first entry)
 XX

DE Bacteriophage Qbeta coat protein mutant Qbeta-259.

XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; anti-inflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; coat protein; mutant; mutein.

OS Synthetic.
 OS Bacteriophage Qbeta.
 PN WO2003059386-A2.

PD 24-JUL-2003.
 XX

PF 17-JAN-2003; 2003WO-BP000460.
 XX

PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (BAACHMANN) BAACHMANN M.
 PA (PELLEICOLI) PELLEICOLI E.
 PA (RENNER) RENNER W.A.
 DR WPI: 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.

Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

Example 1; SEQ ID NO 27; 246pp; English.

This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (Prp) or its dimer, or a Prp peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is the amino acid sequence of a mutant coat protein from bacteriophage Qbeta which may be used during the creation of the vaccine composition of the invention.

Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71; Mismatches 0; Indels 0; Gaps 0;
Matches 132; Conservative 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNKX 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNKX 60
QY 61 NYKQVQKIQNPACTCANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
DB 61 NYKQVQKIQNPACTCANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 7
ADJ82060
ID ADJ82060 standard; protein; 132 AA.

AC ADJ82060;
DT 06-MAY-2004 (first entry)
DE Protein for RANKL antigen array to treat bone disease.
KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.
OS Unidentified.
PN WO2003039225-A2.
PD 15-MAY-2003.
PE 07-NOV-2002; 2002MO-EP012449.
PF 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002MO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Bachmann M, Maurer P, Spohn G;
DR WPI; 2003-441430/41.
PT New compositions comprising a core particle and at least one antigen or
PT antigenic determinant, useful for as a vaccine or prophylaxis
PT of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 27; 222pp; English.

The invention relates to a composition comprising a core particle having at least one first attachment site, and at least one antigen or antigenic determinant having at least one second attachment site. The antigen or antigenic determinant is a RANKL protein, RANKL fragment or RANKL peptide. The second attachment site is (non-) naturally occurring with the antigen or antigenic determinant, and is capable of association to the first attachment site. The antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful as a medicament, or for the manufacture of a medicament for treating bone diseases. The composition is especially useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies, and for stimulating mammalian immune system. This sequence represents a protein of the invention.

Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71; Mismatches 0; Indels 0; Gaps 0;
Matches 132; Conservative 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNKX 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNKX 60
QY 61 NYKQVQKIQNPACTCANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
DB 61 NYKQVQKIQNPACTCANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 8
ADK17148
ID ADK17148 standard; peptide; 132 AA.

AC ADK17148;
DT 06-MAY-2004 (first entry)
DE Virus-like particle repetitive antigen array peptide #27.
KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
KW interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
OS Unidentified.
PN WO2003040164-A2.
PD 15-MAY-2003.
PE 07-NOV-2002; 2002MO-EP012455.
PF 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002MO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Bachmann M, Jennings G, Sonderregger I;
DR WPI; 2003-441518/41.
PT Composition comprising an ordered and repetitive antigen or antigenic
PT determinant array, useful as a medicament, or for manufacturing a
PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's Lymphoma.
XX
XX Disclosure; SEQ ID NO 27; 245pp; English.
PS
XX
XX The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive interact array. The
CC compositions are useful as medicaments, or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSQPSRNRK 60
DB 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSQPSRNRK 60
QY 61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTIELAALLASPL 120
DB 61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTIELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132
RESULT 9
ADJ36317
ID ADJ36317 standard; protein; 132 AA.
XX
XX ADJ36317;
XX
XX 22-APR-2004 (first entry)
XX
XX Bacteriophage Qbeta coat protein virus-like particle mutant K2RKL6R.
XX
XX antiallergic; cytosstatic; virucide; immunostimulant; vaccine;
XX immune response; virus-like particle; immunostimulatory; allergy; tumour;
XX chronic disease; chronic viral disease; bacteriophage Qbeta;
XX coat protein; VLP; adjuvant; mutant; mutein.
XX
XX Bacteriophage Qbeta.
XX
XX WO2004000351-A1.
XX
XX 31-DEC-2003.
XX
XX 20-JUN-2003; 2003WO-EP006541.
XX
XX 20-JUN-2002; 2002US-0389898P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann MF, Renner WA;
XX
XX WPI; 2004-108361/11.
XX
XX New compositions comprising a virus-like particle (VLP), an
XX immunostimulatory substance bound to the VLP, and an antigen mixed with
XX the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
XX Disclosure; SEQ ID NO 18; 252pp; English.
PS
XX
XX The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
CC coat protein mutant, a virus like particle (VLP) that can be used in the
CC adjuvant of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSQPSRNRK 60
DB 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSQPSRNRK 60
QY 61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTIELAALLASPL 120
DB 61 NYKVQVKIQNPPTACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTIELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132
RESULT 10
ADJ67163
ID ADJ67163 standard; protein; 132 AA.
XX
XX ADJ67163;
XX
XX 06-MAY-2004 (first entry)
XX
XX Phage Qbeta coat protein mutant Qbeta 259 for antigen display array.
XX
XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
XX antigenic array.
XX
XX Bacteriophage Qbeta.
XX
XX Synthetic.
XX
XX WO2004009124-A2.
XX
XX 29-JAN-2004.
XX
XX 18-JUL-2003; 2003WO-EP007849.
XX
XX 19-JUL-2002; 2002US-0396638P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann MF, Fulurija A;
XX
XX WPI; 2004-132866/13.
XX
XX New composition comprising a core particle having a first attachment site
XX and an antigen or antigenic determinant which is a ghrelin or ghrelin
XX peptide having a second attachment site, useful for treating obesity.
XX
XX Disclosure; SEQ ID NO 21; 175pp; English.
XX
XX The invention relates to a new composition comprising: (1) a core
XX particle with at least one first attachment site; and (1i) at least one
XX antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
CC peptide, and where the second attachment site being consisting of an
CC attachment site not naturally occurring with the antigen or antigenic
CC determinant and an attachment site naturally occurring with the antigen
CC or antigenic determinant, where the second attachment site is capable of
CC association to the first attachment site, and where the ghrelin or a
CC ghrelin peptide and the core particle interact through the association to
CC form an ordered and repetitive antigen array. The composition is useful
CC for treating obesity. The repetitive array may form part of a phage or
CC bacterial display array. This peptide corresponds to a Bacteriophage
CC Qbeta coat protein mutant which can used as part of the repetitive or
CC antigenic array.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132
RESULT 11
ADKS2197
ID ADKS2197 standard; protein; 132 AA.
XX
AC ADKS2197;
XX
DT 20-MAY-2004 (first entry)
XX
DE Bacteriophage Qbeta coat protein mutant K2R K16R.
XX
KW neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
KW coat protein; CP; mutant; muttein.
XX
OS Bacteriophage Qbeta.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Misc-difference 2
FT Misc-difference 16 /note= "Wild type Lys substituted by Arg"
FT /note= "Wild type Lys substituted by Arg"
XX
PN WO2004016282-A1.
XX
PD 26-FEB-2004.
XX
PF 18-JUL-2003; 2003WO-EP007864.
XX
PR 19-JUL-2002; 2002US-0396639P.
PR 15-MAY-2003; 2003US-0470432P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
XX
PI Bachmann MF, Tisot A, Ortman R, Luegend R, Staufenbiel M;
PI Frey P;
XX
DR WPI; 2004-203731/19.
XX
PT Composition comprising a core particle with at least one attachment site,

PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
PT such as Alzheimer's disease.
XX
XX
PS Example 1; SEQ ID NO 21; 184pp; English.
XX
CC The invention describes a novel composition comprising a virus-like core
CC particle with at least one attachment site, and an antigenic amyloid beta
CC 1-6 peptide. The new composition comprises: a core particle with at least
CC one first attachment site; and at least one antigen or antigenic
CC determinant with at least one second attachment site, where the antigen
CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
CC second attachment site comprises: an attachment site not naturally
CC occurring with the antigen or antigenic determinant; or an attachment
CC site naturally occurring with the antigen or antigenic determinant. The
CC second attachment site is capable of association to the first attachment
CC site and the beta 1-6 peptide and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC composition is useful for the manufacture of a medicament for treating
CC Alzheimer's disease and related diseases. This is the amino acid sequence
CC of an RNA bacteriophage Qbeta coat protein mutant that can be used in the
CC preparation of the compositions and vaccines of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132
RESULT 12
ABG94320
ID ABG94320 standard; protein; 132 AA.
XX
AC ABG94320;
XX
DT 29-AUG-2003 (revised)
DT 10-DEC-2002 (first entry)
XX
DE PQB251 protein.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
OS unidentified bacteriophage.
XX
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-1B000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0286549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tisot A, Maurer P, Lechner F, Seibel P;
PI Plossek C;

XX WPI; 2002-627351/67.
 XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX Claim 18; Page 426; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytoprotective,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS-field)
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 4.5e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLETVTLNIGKDGQTLVLRNPNVNGVSLSOAGVPLAEKRVTVSVQSPRNK 60
 Db 1 AKLETVTLNIGKDGQTLVLRNPNVNGVSLSOAGVPLAEKRVTVSVQSPRNK 60
 QY 61 NYKVVQKIQNPACTANGSCDPSVTROKADVTFSFQVSTDEBERAFVETELAAALASP 120
 Db 61 NYKVVQKIQNPACTANGSCDPSVTROKADVTFSFQVSTDEBERAFVETELAAALASP 120
 QY 121 LIDAIQOLNPAY 132
 Db 121 LIDAIQOLNPAY 132
 QY 121 LIDAIQOLNPAY 132
 Db 121 LIDAIQOLNPAY 132
 RESULT 13
 ABG80632
 ID ABG80632 standard; protein; 132 AA.
 AC ABG80632;
 XX
 XX 29-NOV-2002 (first entry)
 XX
 DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-259.
 XX
 XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease; lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KW enterokinase; cysteine-containing linker.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 XX 21-JAN-2002; 2002WO-1B000168.
 PF
 XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTW/) ORTMANN R.
 PA (LUBO/) LUBOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P., Lechner F., Ortmann R., Lueoend R., Staufenbiel M., Frey P;
 PI Renner WA., Bachmann M., Tissot A., Sebbel P., Ploesek C;
 XX
 XX WPI; 2002-636514/68.
 DR
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 PS
 PS Example 18; Page 146; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative disease lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 CC
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 4.5e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTYLGNGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60
Db 1 AKLEVTYLGNGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTRANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTRANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Qy 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 14
ABR56455
ID ABR56455 standard; protein; 132 AA.
AC ABR56455;
XX 28-JUL-2003 (first entry)
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:26.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW cytosolic; virucide; antibacterial; antiparasitic; fungicide;
KW antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
KW antihydroid; antidiabetic; neuroprotective; nootropic; osteopathic;
KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KW graft-verus-host disease; Grave's disease; diabetes; multiple sclerosis;
KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KW inflammatory autoimmune disease.
XX
XX Bacteriophage Qbeta.
OS Synthetic.
OS WO2003024480-A2.
XX
XX 27-MAR-2003.
PD 16-SEP-2002; 2002MO-IB004252.
XX
XX 14-SEP-2001; 2001US-0318967P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA Bachmann MF, Storni T, Lechner F;
PI WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 182; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
CC antihydroid, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an

CC animal, enhancing anti-viral protection in an animal, or immunizing or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-verus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69852 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ
Query Match 99.5%; Score 661; DB 6; Length 132;
Best Local Similarity 99.2%; Pred. No. 4,5e-71;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARLEVTYLGNGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60
Db 1 AKLEVTYLGNGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTRANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTRANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Qy 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 15
ABU09693
ID ABU09693 standard; protein; 132 AA.
XX
XX ABU09693;
AC
XX
XX 03-JUL-2003 (first entry)
DE Bacteriophage Qbeta mutant coat protein #5.
XX
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
KW cardiant; nephroprotectic; ophthalmological; immunostimulant; vaccine;
KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KW renin-activated angiotensin system; hypertension; stroke; infarction;
KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
KW mutuin.
XX
XX Bacteriophage Qbeta.
OS
XX
XX WO2003031466-A2.
XX
XX 17-APR-2003.
PD 07-OCT-2002; 2002MO-BP011219.
XX
XX 05-OCT-2001; 2001US-0326998P.
XX
XX 07-NOV-2001; 2001US-0331045P.
XX
XX 18-JAN-2002; 2002US-00050902.
XX
XX 21-JAN-2002; 2002MO-IB000156.
XX
XX 19-JUL-2002; 2002US-0396637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA Bachmann M;
PI WPI; 2003-430264/40.
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
XX Claim 20, Page 94, 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate

comprising: (a) a carrier with at least one first attachment site; and (b) at least one angiotensin peptide moiety with at least one second attachment site. The angiotensin peptide conjugate and compositions comprising them are useful for immunising an animal against an angiotensin peptide, and for treating or preventing a physical disorder associated with renin-activated angiotensin system such as hypertension, stroke, infarction, congestive heart failure, kidney failure, and retinal haemorrhage. The conjugate is also useful for inducing immune responses, including producing antibodies. This is the amino acid sequence of a mutant bacteriophage Qbeta coat protein used in the preparation of the vaccine conjugates of the invention

XX
Sequence 132 AA:

Query Match 99.5%; Score 661; DB 6; Length 132;

Best Local Similarity 99.2%; Pred. No. 4.5e-71;

Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	ARLEVTTLGNIGKDGROTLVLPNRGVNPTNGVASLSQAGAVPALERKVTVSVSQPSRNK	60
Db	1	AKLEIVTLGNIGKDGROTLVLPNRGVNPTNGVASLSQAGAVPALERKVTVSVSQPSRNK	60
QY	61	NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDERAAVRTLEAALIASPL	120
Db	61	NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDERAAVRTLEAALIASPL	120
QY	121	LIDAIQOLNPAY	132
Db	121	LIDAIQOLNPAY	132

Search completed: January 4, 2005, 09:11:02
Job time : 39.6824 secs

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best Local Similarity 22.7%; Pred. No. 0.16; Mismatches 44; Indels 35; Gaps 5;
Matches 30; Conservative 23;

QY 13 KGGRTLV-----NPRGVNPTNGVASLSQAGAVPALEKRV 48
DB 138 KGGRTLV-----NPRGVNPTNGVASLSQAGAVPALEKRV 197
QY 49 TVSVSOPSRNRKRYKQVQKIQNPCTANGSCDPSVTR-----QKADVTSTFTQYSTD 102
DB 198 TVSVSOPSRNRKRYKQVQKIQNPCTANGSCDPSVTR-----QKADVTSTFTQYSTD 252
QY 103 EERAFVTELEA 114
DB 253 DEMATSESLIA 264

RESULT 3

US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562938
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match 12.0%; Score 79.5; DB 4; Length 409;
Best Local Similarity 26.5%; Pred. No. 0.35; Mismatches 53; Indels 25; Gaps 6;
Matches 35; Conservative 19;

QY 7 TLGNIGKDGRTLVN---PR-----GVNPTNGVASLSQAGAVPALEKRVTVSVSOPS 56
DB 109 SLINFTKDVAGGRTLVNVRNRLISFAVVPVGTTP-----IAKPNRRLTTRDLAAG 163
QY 57 RNRKRVKQVQKIQNPCTANGSCDPSVTRKQVADVTSTFTQYSTDEERAFVTELEA 116
DB 164 RTGSN---ALAYIRETGFNNALVPENTAKPSEITP-----BEVNESVTIAHMLK 213
QY 117 ASPLLDALDQL 128
DB 214 ASKQIIDLPLQL 225

RESULT 4

US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match 11.2%; Score 74.5; DB 4; Length 916;
Best Local Similarity 23.7%; Pred. No. 5.3; Mismatches 53; Indels 21; Gaps 4;
Matches 28; Conservative 16;

QY 9 GNIGKDG-----RQTLVNPGRVNPNGVASLSQAGAVPALEKRVTVSVS-----QP 55
DB 789 GNIGKDG-----RQTLVNPGRVNPNGVASLSQAGAVPALEKRVTVSVS-----QP 848
QY 56 SNNRKYKQVQKIQNPCTANGSCDPSVTRKQVADVTSTFTQYSTDEERAFVTE 110
DB 849 SNNRKYKQVQKIQNPCTANGSCDPSVTRKQVADVTSTFTQYSTDEERAFVTE 901

RESULT 5

US-09-045-186-2
Sequence 2, Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-045-186-2

Query Match 10.8%; Score 71.5; DB 3; Length 383;

Best Local Similarity 25.9%; Pred. No. 3.2; Mismatches 34; Indels 35; Gaps 4;

Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVLRGVPNTN-----GVA---SLSQAGAVPALEKRVTVSVSOPSRRNKRYKVQVK 67

DB 138 RHQLINPRGWRPNRHHAYGVIAVWLAVALASLPFLIYQ--VMTDEPRQN----- 186

QY 68 IONPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAAL 115

DB 187 -----VTLDAYKDKYVCFDQPPSDSHRLSYTTLTLVL 218

RESULT 6

US-08-232-144-4

Sequence 4, Application US/08232144

Patent No. 5571695

GENERAL INFORMATION:

APPLICANT: SELBIE, Lisa

APPLICANT: HERZOG, Herbert

TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

STREET: 555 13th St, N.W., Suite 701-Bast

CITY: Washington

STATE: DC

COUNTRY: US

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,144

FILING DATE: 26-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, Barbara G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1871-107A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-232-144-4

Query Match 10.8%; Score 71.5; DB 1; Length 384;

Best Local Similarity 25.9%; Pred. No. 3.2;

Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVLRGVPNTN-----GVA---SLSQAGAVPALEKRVTVSVSOPSRRNKRYKVQVK 67

DB 138 RHQLINPRGWRPNRHHAYGVIAVWLAVALASLPFLIYQ--VMTDEPRQN----- 186

QY 68 IONPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAAL 115

DB 187 -----VTLDAYKDKYVCFDQPPSDSHRLSYTTLTLVL 218

RESULT 7

US-08-555-268A-15

Sequence 15, Application US/08555268A

Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.

APPLICANT: Walker, Mary

APPLICANT: Branchek, Theresa

APPLICANT: Weinshank, Richard L.

TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE

TITLE OF INVENTION: Y/PEPTIDE Y1/PANCREATIC POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/555,268A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44743-Z/JPW/MAT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 391-0526

FAX: (212) 278-0400

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-555-268A-15

Query Match 10.8%; Score 71.5; DB 2; Length 384;

Best Local Similarity 25.9%; Pred. No. 3.2;

Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVLRGVPNTN-----GVA---SLSQAGAVPALEKRVTVSVSOPSRRNKRYKVQVK 67

DB 138 RHQLINPRGWRPNRHHAYGVIAVWLAVALASLPFLIYQ--VMTDEPRQN----- 186

QY 68 IONPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAAL 115

DB 187 -----VTLDAYKDKYVCFDQPPSDSHRLSYTTLTLVL 218

RESULT 8

US-09-200-673-15

Sequence 15, Application US/09200673A

Patent No. 6316203

GENERAL INFORMATION:

APPLICANT: Gerold, Christophe P.G.

APPLICANT: Weinshank, Richard L.

APPLICANT: Walker, Mary W.

APPLICANT: Branchek, Theresa

TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful

TITLE OF INVENTION: in Such Methods, and DNA Encoding A Hypothalamic

FILE REFERENCE: 46166-BZ/JPW

CURRENT APPLICATION NUMBER: US/09/200,673A

EARLIER FILING DATE: 1998-11-25

EARLIER FILING DATE: 1995-12-01

EARLIER APPLICATION NUMBER: 08/349,025

EARLIER FILING DATE: 1994-12-02

NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 15
LENGTH: 384
TYPE: PRF
ORGANISM: Homo sapiens
US-09-200-673-15

Query Match 10.8%; Score 71.5; DB 3; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVPTN-----GVA---SLSQAGVAPLEKRVTVSQQPSRNKRYKVOYK 67
DB 138 RQTLVNPGRVPTNHHAYVGIWVLAASSLPFLIYQ--VMTDEPFQN----- 186

US-10-013-846-4
Sequence 4, Application US/10013846

GENERAL INFORMATION:
APPLICANT: Baktavatchalam, Rajagopal
APPLICANT: Blum, Charles A
APPLICANT: Briemann, Harry L
APPLICANT: Darrow, James W
APPLICANT: De Lombarc, Stephane
APPLICANT: Hutchison, Alan
APPLICANT: Tran, Jennifer
APPLICANT: Zheng, Xiaozhang
APPLICANT: Elliott, Richard L
APPLICANT: Hammond, Mariys
TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
TITLE OF INVENTION: 3H-spiroisobenzofuran-1,4'-piperidines
FILE REFERENCE: N00.2001
CURRENT APPLICATION NUMBER: US/10/013,846
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,990
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln version 3.1
SEQ ID NO 4
LENGTH: 384
TYPE: PRF
ORGANISM: homoeapiens
US-10-013-846-4

Query Match 10.8%; Score 71.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVPTN-----GVA---SLSQAGVAPLEKRVTVSQQPSRNKRYKVOYK 67
DB 138 RQTLVNPGRVPTNHHAYVGIWVLAASSLPFLIYQ--VMTDEPFQN----- 186

US-09-708-392-9
Sequence 9, Application US/09708392

GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Wayman, G

TITLE OF INVENTION: Pharmaceutical
FILE REFERENCE: PC10343AAK
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: GB 9926437.6
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 0004021.2
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 0016563.9
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: GB 0017141.3
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 60/221,014
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/221,093
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 9
LENGTH: 384
TYPE: PRF
ORGANISM: Homo sapiens
US-09-708-392-9

Query Match 10.8%; Score 71.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVPTN-----GVA---SLSQAGVAPLEKRVTVSQQPSRNKRYKVOYK 67
DB 138 RQTLVNPGRVPTNHHAYVGIWVLAASSLPFLIYQ--VMTDEPFQN----- 186

US-09-708-392-9
Sequence 9, Application US/09708392

GENERAL INFORMATION:
APPLICANT: Claes R. Wahlestedt
TITLE OF INVENTION: Human Neuropeptide Y/Peptide YY
TITLE OF INVENTION: Receptor of the Y1-Type and
TITLE OF INVENTION: Antisense Oligonucleotides
TITLE OF INVENTION: Thereto which inhibit Vasoconstriction
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05039
FILING DATE: 19930527
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRP D-1250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 268-1951
TELEFAX: (203) 268-1951
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-05039-3

Query Match 10.8%; Score 71.5; DB 5; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTIVNPGVNPNTN-----GVA---SLSQAGVPALEKRTVSVSQPSRRKNKYQVOK 67
DB 138 RHQLINRGRPNRHHAYVGIWLVAVASSLPFLIYQ--VMTDEPFQ----- 186

QY 68 IONPFACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKYVCFDQPPSPDSHRLSYTTLTLVL 218

RESULT 12

US-08-817-869-3

Sequence 3, Application US/08817869
Patent No. 6001970

GENERAL INFORMATION:

APPLICANT: STRADER, CATHERINE D.

APPLICANT: CASCIERI, MARGARET A.

APPLICANT: MACNEIL, DOUGLAS J.

TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM H. NICHOLSON

STREET: 126 EAST LINCOLN AVENUE

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: US

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,869

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/335,017

FILING DATE: 07-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: NICHOLSON, WILLIAM H.

REGISTRATION NUMBER: 25,147

TELECOMMUNICATION INFORMATION:

TELEPHONE: (732) 594-1348

TELEFAX: (732) 594-4720

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-817-869-3

Query Match 10.8%; Score 71.5; DB 3; Length 411;

Best Local Similarity 25.9%; Pred. No. 3.6;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;
QY 16 RQTIVNPGVNPNTN-----GVA---SLSQAGVPALEKRTVSVSQPSRRKNKYQVOK 67
DB 141 RHQLINRGRPNRHHAYVGIWLVAVASSLPFLIYQ--VMTDEPFQ----- 189

RESULT 13

PCT-US95-14377-3

Sequence 3, Application PC/TUS9514377
GENERAL INFORMATION:

APPLICANT: STRADER, CATHERINE D.

APPLICANT: CASCIERI, MARGARET A.

APPLICANT: MACNEIL, DOUGLAS J.

TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARY A. APOLLINA

STREET: 126 EAST LINCOLN AVENUE

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: US

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14377

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/335,017

FILING DATE: 07-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: APOLLINA, MARY A.

REGISTRATION NUMBER: 34,087

REFERENCE/DOCKET NUMBER: 19339Y PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3462

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-14377-3

Query Match 10.8%; Score 71.5; DB 5; Length 411;
Best Local Similarity 25.9%; Pred. No. 3.6;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTIVNPGVNPNTN-----GVA---SLSQAGVPALEKRTVSVSQPSRRKNKYQVOK 67
DB 141 RHQLINRGRPNRHHAYVGIWLVAVASSLPFLIYQ--VMTDEPFQ----- 189

QY 68 IONPFACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAAL 115
DB 190 -----VTLDAYKDKYVCFDQPPSPDSHRLSYTTLTLVL 221

RESULT 14

US-09-270-767-44620

Sequence 44620, Application US/09270767
Patent No. 6703491

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTYVIGNIGKDGRTLV.....AALISPLLDIDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	14	US-10-243-739-27 Sequence 27, Appl
2	664	100.0	132	14	US-10-244-065-27 Sequence 27, Appl
3	664	100.0	132	14	US-10-288-454-27 Sequence 27, Appl
4	664	100.0	132	14	US-10-050-902-258 Sequence 25, App
5	664	100.0	132	14	US-10-050-898-258 Sequence 25, App
6	664	100.0	132	14	US-10-346-190-27 Sequence 27, Appl
7	664	100.0	132	15	US-10-465-811-18 Sequence 18, Appl
8	664	100.0	132	15	US-10-289-456-27 Sequence 27, Appl
9	664	100.0	132	15	US-10-622-064-10 Sequence 10, Appl
10	664	100.0	132	15	US-10-622-124-21 Sequence 21, Appl
11	664	100.0	132	16	US-10-622-087-21 Sequence 26, Appl
12	661	99.5	132	14	US-10-243-739-26 Sequence 26, Appl
13	661	99.5	132	14	US-10-244-065-26 Sequence 26, Appl

14	661	99.5	132	14	US-10-289-454-26	Sequence 26, Appl
15	661	99.5	132	14	US-10-050-902-259	Sequence 25, App
16	661	99.5	132	14	US-10-050-898-259	Sequence 25, App
17	661	99.5	132	14	US-10-346-190-26	Sequence 26, Appl
18	661	99.5	132	15	US-10-465-811-17	Sequence 17, Appl
19	661	99.5	132	15	US-10-289-456-26	Sequence 26, Appl
20	661	99.5	132	15	US-10-622-064-9	Sequence 9, Appl
21	661	99.5	132	15	US-10-622-124-20	Sequence 20, Appl
22	661	99.5	132	16	US-10-622-087-20	Sequence 20, Appl
23	658	99.1	132	14	US-10-243-739-25	Sequence 25, Appl
24	658	99.1	132	14	US-10-244-065-25	Sequence 25, Appl
25	658	99.1	132	14	US-10-289-454-25	Sequence 25, App
26	658	99.1	132	14	US-10-050-902-257	Sequence 25, App
27	658	99.1	132	14	US-10-050-898-257	Sequence 25, Appl
28	658	99.1	132	14	US-10-346-190-25	Sequence 25, Appl
29	658	99.1	132	15	US-10-465-811-16	Sequence 16, Appl
30	658	99.1	132	15	US-10-289-456-25	Sequence 25, Appl
31	658	99.1	132	15	US-10-622-064-8	Sequence 8, Appl
32	658	99.1	132	15	US-10-622-124-19	Sequence 19, Appl
33	658	99.1	132	16	US-10-622-087-19	Sequence 19, Appl
34	655	98.6	132	14	US-10-243-739-23	Sequence 23, Appl
35	655	98.6	132	14	US-10-244-065-23	Sequence 23, Appl
36	655	98.6	132	14	US-10-289-454-23	Sequence 23, Appl
37	655	98.6	132	14	US-10-050-902-255	Sequence 25, App
38	655	98.6	132	14	US-10-050-898-255	Sequence 25, App
39	655	98.6	132	14	US-10-346-190-23	Sequence 23, Appl
40	655	98.6	132	15	US-10-465-811-14	Sequence 14, Appl
41	655	98.6	132	15	US-10-289-456-23	Sequence 23, Appl
42	655	98.6	132	15	US-10-622-064-6	Sequence 6, Appl
43	655	98.6	132	15	US-10-622-124-17	Sequence 17, Appl
44	655	98.6	132	16	US-10-622-087-17	Sequence 17, Appl
45	652	98.2	132	14	US-10-243-739-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-243-739-27
Sequence 27, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Frankiska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2001-09-14
PRIORITY FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-27
Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLEVTYVIGNIGKDGRTLVLPNGVNPNGVYASLSQAGVPALEKRTVSVSQSRNRK 60
1 ARLEVTYVIGNIGKDGRTLVLPNGVNPNGVYASLSQAGVPALEKRTVSVSQSRNRK 60
DB 1 ARLEVTYVIGNIGKDGRTLVLPNGVNPNGVYASLSQAGVPALEKRTVSVSQSRNRK 60
QY 61 NKVVQVKNPACTANGSCDPSVTRKQADVTFSFTQSTDEBPAFRTIELAALLASPL 120
61 NKVVQVKNPACTANGSCDPSVTRKQADVTFSFTQSTDEBPAFRTIELAALLASPL 120
DB 61 NKVVQVKNPACTANGSCDPSVTRKQADVTFSFTQSTDEBPAFRTIELAALLASPL 120
QY 121 LIDAIDQLNPAY 132

Db 121 LIDAIQOLNPAY 132

RESULT 2

US-10-244-065-27
; Sequence 27, Application US/10244065
; Publication No. US20030095668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tisot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Mejerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Induls
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-Like Particles
; FILE REFERENCE: 1700.022001
; CURRENT APPLICATION NUMBER: US/10/244,065
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-27

Query Match 100.0%; Score 664; DB 14; Length 132;

Best Local Similarity 100.0%; Pred. No. 1,66-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGKDGKQRTLVLPNGVPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
Db 1 ARLEVTTLGNIGKDGKQRTLVLPNGVPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 3

US-10-289-454-27
; Sequence 27, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.036001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta-259
US-10-289-454-27

Query Match 100.0%; Score 664; DB 14; Length 132;

Best Local Similarity 100.0%; Pred. No. 1,66-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGKDGKQRTLVLPNGVPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
Db 1 ARLEVTTLGNIGKDGKQRTLVLPNGVPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 4

US-10-050-902-258
; Sequence 258, Application US/1005902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.019004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
US-10-050-902-258

Query Match 100.0%; Score 664; DB 14; Length 132;

Best Local Similarity 100.0%; Pred. No. 1,66-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGKDGKQRTLVLPNGVPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
Db 1 ARLEVTTLGNIGKDGKQRTLVLPNGVPTNGVASLSQAGAVPALEKRTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 5
US-10-050-898-258
; Sequence 258, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050.898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 258
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
US-10-050-898-258

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTYIGNIGKGRQTLVNPGRVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60
Db 1 ARLEVTYIGNIGKGRQTLVNPGRVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60

Qy 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRETELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRETELAALLASPL 120

Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 6
US-10-346-190-27
; Sequence 27, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pellicioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346.190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 27
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
US-10-346-190-27

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTYIGNIGKGRQTLVNPGRVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60
Db 1 ARLEVTYIGNIGKGRQTLVNPGRVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60

Qy 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRETELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRETELAALLASPL 120

Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 7
US-10-465-811-18
; Sequence 18, Application US/10465811
; Publication No. US2004000538A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465.811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 18
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
US-10-465-811-18

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTYIGNIGKGRQTLVNPGRVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60
Db 1 ARLEVTYIGNIGKGRQTLVNPGRVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60

Qy 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRETELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRETELAALLASPL 120

Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 8
US-10-289-456-27
; Sequence 27, Application US/10289456

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; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurel, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Q-beta 259 mutant
; US-10-289-456-27
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Query Match          100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1,6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY      121 LIDAIDQLNPAY 132
DB      121 LIDAIDQLNPAY 132
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RESULT 9
US-10-622-064-10
; Sequence 10, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurel, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
; US-10-622-064-10
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Query Match          100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1,6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
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DB      1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
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DB      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY      121 LIDAIDQLNPAY 132
DB      121 LIDAIDQLNPAY 132
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```
RESULT 10
US-10-622-124-21
; Sequence 21, Application US/10622124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Pulurija, Alma
; TITLE OF INVENTION: Ghrelin-Carrier Conjugates
; FILE REFERENCE: 1700.0340001
; CURRENT APPLICATION NUMBER: US/10/622,124
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,638
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
; US-10-622-124-21
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Query Match          100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1,6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB      1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB      61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY      121 LIDAIDQLNPAY 132
DB      121 LIDAIDQLNPAY 132
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```
RESULT 11
US-10-622-087-21
; Sequence 21, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
; FILE REFERENCE: 1700.0350002
; CURRENT APPLICATION NUMBER: US/10/622,087
; CURRENT FILING DATE: 2003-07-19
; PRIOR APPLICATION NUMBER: US 60/396,639
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/470,432
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
```

LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
US-10-622-087-21

Query Match 100.0%; Score 664; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60
DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFYRTTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFYRTTELAALLASPL 120
QY 121 LIDAIDQLNPAV 132
DB 121 LIDAIDQLNPAV 132

RESULT 12
US-10-243-739-26
Sequence 26, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-26

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60
DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFYRTTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFYRTTELAALLASPL 120
QY 121 LIDAIDQLNPAV 132
DB 121 LIDAIDQLNPAV 132

RESULT 13
US-10-244-065-26
Sequence 26, Application US/10244065
Publication No. US20030099668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tisbet, Alain

APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-26

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60
DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFYRTTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAFYRTTELAALLASPL 120
QY 121 LIDAIDQLNPAV 132
DB 121 LIDAIDQLNPAV 132

RESULT 14
US-10-289-454-26
Sequence 26, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-251
US-10-289-454-26

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASISQAGAVPALERKRVTSVSQPSRRNK 60

Db 1 AKLEVTTLGNIGKDGROTLVLPNGVNPINGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTEIAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTEIAALLASPL 120
QY 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 15

US-10-050-902-259
Sequence 259, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tisbet, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Seibel, Peter
APPLICANT: Plosek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 259
LENGTH: 132
TYPE: PRT
ORGANISM: Qb 251
US-10-050-902-259

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPINGVASLSQAGAVPALERKVTVSQPSRNRK 60
Db 1 AKLEVTTLGNIGKDGROTLVLPNGVNPINGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTEIAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTEIAALLASPL 120
QY 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

Search completed: January 4, 2005, 09:41:23
Job time: 32.7351 secs

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

```

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTLTGNIGKDGRTLV.....AALLASPLUIDAIDQNPAY 132

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

```
Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	652	98.2	132	1	VCBPB	coat protein - phage
2	528.5	79.6	331	2	S01964	readthrough protease
3	116	17.5	131	1	VCBPB1	coat protein - phage
4	89.5	13.5	530	2	S22340	seeligertolysin -
5	85.5	12.9	540	2	T00646	hypothetical protein
6	84.5	12.7	529	2	S24231	hypothetical protein
7	84.5	12.7	529	2	A43505	hypothetical protein
8	84.5	12.7	529	2	AC1100	hypothetical protein
9	80.5	12.1	528	2	S22341	hypothetical protein
10	80.5	12.1	1502	1	RCBHY1	hypothetical protein
11	79	11.9	282	2	A10186	probable iron-sulfur
12	79	11.9	432	2	T13660	hypothetical protein
13	78.5	11.8	1861	2	T13845	microtubule-associated
14	78	11.7	830	2	S57537	MKT1 protein - yeast
15	76.5	11.5	136	2	C98221	hypothetical protein
16	76.5	11.5	136	2	AE3065	hypothetical protein
17	76.5	11.5	1052	2	C64221	conserved hypothetical
18	75.5	11.4	1097	2	AD2572	hypothetical protein
19	75	11.3	130	1	A46374	hypothetical protein
20	75	11.3	130	1	VCBPB4	coat protein - phage
21	74.5	11.2	130	1	VCBPB8	coat protein - phage
22	74.5	11.2	161	4	I55480	hypothetical protein
23	74	11.1	340	2	S18650	hypothetical protein
24	74	11.1	340	2	A42008	hypothetical protein
25	73.5	11.1	191	2	H90078	homeotic protein
26	73.5	11.1	520	1	ACMSD1	hypothetical protein
27	73.5	11.1	601	2	A55971	nicotinic acetylcholine
28	73.5	11.1	719	2	T139271	serine/threonine kinase
29	73	11.0	430	2	G88864	conserved hypothetical protein K09511.10

30	72.5	10.9	129	1	VCBPF	coat protein - pha
31	72.5	10.9	129	1	VCBPF	coat protein - pha
32	72.5	10.9	129	1	VCBPF	coat protein - pha
33	72	10.8	376	2	C84316	hypothetical prote
34	71.5	10.8	384	2	A45490	neuropeptide y/pep
35	71	10.7	248	2	A66786	conserved hypothet
36	71	10.7	399	1	A43685	polymerase-associat
37	71	10.7	463	2	S00676	translacion elonga
38	71	10.7	1461	2	B90696	hypothetical prote
39	71	10.7	1461	2	A85547	hypothetical prote
40	71	10.7	1545	2	T42751	sulfonylurea recep
41	71	10.7	1545	2	T46645	sulfonylurea recep
42	71	10.7	1545	2	T46645	conserved hypothet
43	70.5	10.6	836	2	A13237	conserved hypothet
44	70	10.5	243	1	VHVUP	nucleosidase prote
45	69.5	10.5	425	2	S69796	pectate lyase (EC
45	69.5	10.5	130	1	VCBPM2	coat protein [vali

ALIGNMENTS

RESULT 1

coat protein phage O-beta
C:Species: phage O-beta
C:Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #ext_change 09-Jul-2004
C:Accession: A92240; A92221; A92088; A04224
R:Escarmls, C.; Sastry, P.A.; Billeter, M.A.
J. Biol. Chem. 253, 8390-8399, 1978
A:Title: Determination of the first half of the coat protein clefton of bacteriophage Qbeta
A:Reference number: A92240; MUID:79048469; PMID:361741
A:Accession: A92240
A:Molecule type: mRNA
A:Residues: 1-80 <ESC>
A:Cross-references: UNIPROT:P03615
R:Stoll, E.; Wilson, K.J.; Reiser, J.; Weissmann, C.
J. Biol. Chem. 252, 990-993, 1977
A:Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.
A:Reference number: A92221; MUID:77118576; PMID:838709
A:Accession: A92221
A:Molecule type: Protein
A:Residues: 1-60 <STO>
R:Malta, T.; Konigsberg, W.
J. Biol. Chem. 246, 5003-5024, 1971
A:Title: The amino acid sequence of the Qbeta coat protein.
A:Reference number: A92088; MUID:71288580; PMID:5570434
A:Accession: A92088
A:Molecule type: Protein
A:Residues: 1-21, 'D', 23-55, 57-132 <WAI>
C:Superfamily: phage GA coat protein

Query Match 98.2%; Score 652; DB 1; Length 132;
 Query Similarity 97.7%; Pred. No. 1 6e-56;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0.

Qy	1	ARETETTTGNICDKORQTLVYNPBGVNPNTNGVASLSOAGVPALEKXVTYVSOSPNNRK	60
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	1	AKLEIYETLTANICKDKQTLVYNPBGVNPNTNGVASLSOAGVPALEKXVTYVSOSPNNRK	60
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Qy	61	NYKVQYKIONPACTANGSCDPSVYRQCKADVTFSFTQYSTDERAFVRETELAAALLASPL	120
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	61	NKVQYKIONPACTANGSCDPSVYRQAYADVTFSFTQYSTDERAFVRETELAAALLASPL	120
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Qy	121	LIDAIQOLNPAY	132
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	121	LIDAIQOLNPAY	132

RESULT 2

```
readthrough protein - phage SP
C:Species: phage SP
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
```

C:/Accession: S01964
R:Inokuchi, Y.; Jacobson, A. B.; Hirose, T.; Inayama, S.; Hirashima, A.
Nucleic Acids Res. 16, 6205-6221, 1988
A>Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP.
A/Reference number: S01963; MUID:88289362; PMID:3395390
A/Accession: S01964
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-331 <INO>
A/Cross-references: UNIPROT:P09677; EMBL:X07489
A>Note: the authors translated the readthrough stopcodon TGA for residue 133 as Trp
C:Superfamily: phage GA coat protein

Query Match
Best Local Similarity 79.6%; Score 528.5; DB 2; Length 331;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLETTVLGNIGKDGROTLVINPRGVNPTNGVASHISQAGVPALEKRYTVSVSOPSRNRK 60
Db 2 AKLNQVTLSTKIGKNDQTLTPRGVNPPTNGVASHISQAGVPALEKRYTVSVSOPSRNRK 61

QY 61 NYKQVVKQNTACTANGSCDPSVTROKAYVTSFQYSDDERAFRTLAALLASPLLI 120
Db 62 NFKQVVKQNTACTACRD-ACDPSVTRSAFADVTLSTFISYTDDEKALRTLAALLADPL 120

QY 121 LIDAIQINPAY 132
Db 121 IVDAIQINPAY 132

RESULT 3
VCBPPI
coat protein - phage PRRI
C/Species: phage PRRI
C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
A/Accession: A04225
R:Daesele, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
Eur. J. Biochem. 94, 375-386, 1979
A>Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage phi-X174
A/Reference number: A04225; MUID:79148387; PMID:107028
A/Accession: A04225
A/Molecule type: protein
A/Residues: 1-131 <DHA>
A/Cross-references: UNIPROT:P03616
C:Superfamily: phage GA coat protein

Query Match
Best Local Similarity 17.5%; Score 116; DB 1; Length 131;
Matches 42; Conservative 14; Mismatches 56; Indels 16; Gaps 5;

QY 17 QTVLIVNRGVNPT-----NGVASLSQAGVPALEKRYTVSVSOPSRNRKRYKQV 66
Db 4 QNVLVKQREATPNDHTFVPRDIRDQNVGEVSTGVPIGESRFTLSLRKTSNGR--YKSTL 61

QY 67 KIQNPV--ACTANGSCDPSVTROKAYVTSFQYSDDEER-AFVRTLAALLASPLLI- 122
Db 62 KLVVFPVQSQVNGEIVTPVVRTSYTVYDFDYDARSTKENNFTGMIADALKADMLVH 121

QY 123 DAIDQINPAY 132
Db 122 DTIVNLQGVY 131

RESULT 4
S22340
seeligeriolysin - Listeria seeligeri
C/Species: Listeria seeligeri
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: S22340
R:Haas, A.; Dumbeky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A>Title: Listeriolysin genes: complete sequence of ilo from Listeria ivanovi and of lsc

A:Accession: S223340
A>Status: preliminary
Molecule type: DNA
A.Residues: 1-530 <HAA>
A.Cross-references: UNIPROT:P31830; EMBL:X60462; NID:g944144; PIDN:CAA42996.1; PID:g944145
A.Note: the authors translated the codon GCC for residue 287 as Pro

C:Superfamily: dipeptide transport protein

Query Match 13.5%; Score 89.5; DB 2; Length 530;
Best Local Similarity 25.0%; Pred. No. 0.71;
Matches 34; Conservative 22; Mismatches 37; Indels 43; Gaps 7;

OY 13 KDGROTLVLV--NPRGVNP-----NGVASLSQAGA-----VPALERKV 48
 |||:::||:||||:
DB 94 KDGEIIVVEKKKKGNONNADISVINAISSLYPALVKANRELVENGPVLPVKDSDL 153

OY 49 TVSVSOPSRNRKNKYQVQKIONFTACTANGSCDSPSTR--OKY-----ADVTFSTQ 98
 |||:::||:||||:
DB 154 TLTVPLPGMTTKDNKIIFVK--NPTKSNNVANVTLVERNMDKSKAYPNINAKIDYS--- 208

OY 99 YSTDERRAPVRTELAA 114
 ::||:|
DB 209 ----DEMAYSQSOLTA 220

RESULT 5

T00646
hypothetical protein F316_9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00646
R:Federapfel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,
J.; Vysotskaya, V.S.; Yu, G.; Becker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998
A.Reference number: Z14197
A:Accession: T00646
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-540 <FEED>
A.Cross-references: UNIPROT:Q48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g28223
C.Genetics:

A:Gene: ATSP:F316_9
A.Map position: 1
A.Introns: 14/3; 428/3; 448/2; 483/3; 502/3
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binding

Query Match 12.9%; Score 85.5; DB 2; Length 540;
Best Local Similarity 26.1%; Pred. No. 1.8;
Matches 30; Conservative 15; Mismatches 55; Indels 15; Gaps 3;

OY 11 IGDKGRQTILVNPRG--VNPTNGVASLSQAGAVPALERKRYTWSVSOPSNRKN-YRVQV 66
 |||:::||:||||:
DB 255 VKKEKKPMLIKNDGNVRLNTPRGSLKPQVGKPEPNTKTITSRKTPPSKMKMMKATK 314

OY 67 KIQNLTACTANGSCDSPSTRQKADVFSTFYQSTDEBRFAVRTLAALLASPLL 121
 |||:::||:||||:
DB 315 KPAPMSWSPSGFATPRPYKPAPTKTSLSHSLSLKCK-----VSPILL 358

RESULT 6

S24231
Listeriolyisin precursor - Listeria monocytogenes (strain 12067)
C:Species: Listeria monocytogenes
A.Variety: strain 12067
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S24231
R:Ramussen, O.F.; Beck, T.; Olsen, J.E.; Doms, L.; Rossen, L.
Infect. Immun. 59, 3945-3951, 1991
A>Title: Listeria monocytogenes isolates can be classified into two major types according
A.Reference number: S24230; MID:92040062; PMID:1937753
A:Accession: S24231
A.Status: nucleic acid sequence not shown; translation not shown
Molecule type: DNA

C:/Superfamily/dipeptide transport protein
C:/Keywords: virulence factor
F:/1-25/Domain: signal sequence #status predicted <Sig>
F:/26-529/Product: Listeriolysin O #status predicted <Mat>

Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

Dy 13 KDGQRTLVL-----NPRGVPTNGVASLSQAQA-----VPALEKRV 48
||| : : : ||
Dd 93 KDGNRYIVAEKKKKKSINQNNAADIQVNVAISSLTYPALVYKANSELYENQPDVLVPVRDSL 152

Dy 49 TVSVSQPSRRNRKYKVQVKIQNPFACTANGSCDPSTVR-----QRYADVFESFTGYSTD 102
||| : : : ||
Db 153 TLSIDILPGMTNQDNKIYVK--NATKSNVVNNAVTLVERWNEKYAQAYPNVS---AKIDVD 207

Dy 103 EERAFVRTIELAA 114
: | : : : |
Db 208 DEMAYSQSOLIA 219

RESULT 8
AC1100
Listeriolysin O precursor [imported] - Listeria monocytogenes (strain EGD-e)
C:/Species: Listeria monocytogenes
C:/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #ext_change 09-Jul-2004
C:/Accession: AC1100
R;/Glaser, P.; Frangoull, L.; Buchrieser, C.; Amend, A.; Baguerio, F.; Berche, P.; Blocker,
J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:/Authors: Kreft, J., Kim, W., Kunst, F., Kurapkut, G., Madueno, E., Maitournam, A.; Ma
ok, C.; Schluter, T.; Simes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A./Title: Comparative genomics of Listeria species.
A:/Reference number: AB1077; PMID:21537279; PMID:11679669
A:/Accession: AC1100
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-529 <GLA>
A:/Cross-references: UNIPROT:P13128; GB:NC_003210; PIDB:CAD00729.1; PID:gl6409567; CASPDB:
A:/Experimental source: strain EGD-e
C:/Genetic:
A:/Gene: hly
C:/Superfamily: dipeptide transport protein

Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

Dy 13 KDGQRTLVL-----NPRGVPTNGVASLSQAQA-----VPALEKRV 48
||| : : : ||
Dd 93 KDGNRYIVAEKKKKKSINQNNAADIQVNVAISSLTYPALVYKANSELYENQPDVLVPVRDSL 152

Dy 49 TVSVSQPSRRNRKYKVQVKIQNPFACTANGSCDPSTVR-----QRYADVFESFTGYSTD 102
||| : : : ||
Db 153 TLSIDILPGMTNQDNKIYVK--NATKSNVVNNAVTLVERWNEKYAQAYPNVS---AKIDVD 207

Dy 103 EERAFVRTIELAA 114
: | : : : |
Db 208 DEMAYSQSOLIA 219

RESULT 9
S22341
Ivanomycin precursor - Listeria ivanovi
C:/Species: Listeria ivanovi
C:/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #ext_change 09-Jun-2004
C:/Accession: S22341; S36683
R;/Haas, A.; Dumbaky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:/Title: Listeriolysin genes: complete sequence of llo from Listeria ivanovi and of lso
A:/Reference number: S22340; MOID:p2182018; PMID:1543752

A:Accession: S22341
A:Molecule type: DNA
A:Residues: 1-528 <HAS>
A:Cross-references: UNIPROT:P31831; EMBL:X60461
A>Note: The authors translated the codon ACA for residue 331 as Val R:kref, J.
submitted to the EMBL Data Library, July 1991
A:Reference number: S36683
A:Accession: S36683
A:Molecule type: DNA
A:Residues: 1-319,'T',321-528 <KRE>
A:Cross-references: EMBL:X60461
C:Genetics:
A:Gene: ilo
C:Superfamily: dipeptide transport protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-528/Product: Ivaolysin #status predicted <MAT>

Query Match 12.1% Score 80.5; DB 2; Length 528;
Best Local Similarity 22.0%; Pred. No. 5.3;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

OY 13 KDGQTVTL-----NPRGVNPTNGASISQAGA-----VPALEKRV 48
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 92 KEGNQYIVVEKKKSINGNADIQYNISLASLTYPGALVKANSELVENQPVLVKKDSV 151
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 49 TVSVSQSPERNKNKYQVQKIONPFACTANGSCDPSVTR-----OKTADVTFSTGYSTD 102
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 152 TLSDILP--GMVNHDNEIIVONATKSNINDGVNTLVDRMNNKYSBEVPNIS---AKIDYD 206
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 103 EERAFVETELAA 114
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 207 QEMAISESQIVA 218

RESULT 10
RGBHYH1
CYCL/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L9672.1; protein YLR256w; regulatory protein CYP1; regulatory
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1991 #sequence revision 23-Feb-1996 #text_change 12-Nov-1999
C:Accession: S59400; A13132; S15447; S05804; S15446
R:Johnson, D.
submitted to the EMBL Data Library, February 1995
A>Description: The sequence of S. cerevisiae cosmid 9672.
A:Reference number: S59386
A:Accession: S59400
A:Molecule type: DNA
A:Residues: 1-1502 <JOH>
A:Cross-references: EMBL:U20865; NID:g662330; PIDN:AAB67387.1; PID:g662331; GSPDB:GN0007
A:Experimental source: strain S288C (AB972)
R:Pfeiffer, K.; Kim, K.S.; Kogan, S.; Quarente, L.
Cell 56, 291-301, 1989
A>Title: Functional dissection and sequence of yeast HAP1 activator.
A:Reference number: A13132; MUID:89106221; PMID:2643482
A:Accession: A13132
A:Molecule type: DNA
A:Residues: 1-144,'I',146-322,'R',324-454,'N',456-507,'W',509-586,'K',588-882,'N',884-95
A:Cross-references: EMBL:J03152; NID:g171645; PIDN:AAA34662.1; PID:g171646
R:Crusset, F.; Verdier, J.; Gaisne, M.; Slonimski, P.P.
J. Mol. Biol. 204, 263-276, 1988
A>Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
A:Reference number: S15447; MUID:89125585; PMID:2851658
A:Accession: S15447
A:Molecule type: DNA
A:Residues: 1-62,'R',64-1305,'Y',1306-1470,'LVDFRADFPIME' <CRE1>
A:Cross-references: EMBL:X13793
A>Note: The sequence is from mutant CYP1-18
C:Genetics:
A:Gene: SGD:HAP1; CYP1; MIPS:YLR256w
A:Cross-references: SGD:S0004246; MIPS:YLR256w
A:Map position: 12R
C:Superfamily: regulatory protein HAP1, GAL4 zinc binuclear cluster homology

C;Keywords: DNA binding; heme binding; transcription regulation; zinc finger
F.1-148/Domain: DNA binding #status predicted <DNA>
P.159-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F.64-84/Region: zinc finger CCCC motif
F.177-189/Region: glutamine-rich
P.245-445/Domains: heme binding #status predicted <HEM>
F.1299-304,333-328,373-352,373-378,389-394,415-420/Region: 6-residue repeats
F.1308-1481/Domains: activation element #status predicted <ACT>
F.1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
Best Local Similarity 20.6%; Pred. No. 18;
Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;

OY 23 PRGVN--PNGVSL-----SOAGVPALERVTVSYS 53
|||:::||:::
Db 1278 PGGSPKDSNGLSQWPLISSFSMNQLNGTTPPSLNTISQMGLPSIDRTTNQIN 1337
|||||
OY 54 QSRNR-KNYKVQNQP-----TACANGSCP 82
||::|:
Db 1338 LPDRSDERFDNSIKOMTWTSAPMANATTIPSTLANGNMNNMGATPAINDTSSANGSALS 1397
|||:
OY 83 SVTRCKADV-TFSFTYSTD-EERAFAVETELALLASP-LIIDAIDLNL 129
::||::|:
Db 1398 TLTSQGSGDLASNSATQVKPDLEDFLMQNSNFGLMINPFSELVEVGYN 1447

RESULT 11
A10186
Probable iron-siderophore transport system, ATP-binding component YPO15j3 [imported] - Yeast
CSpecies: Yerishia pestis
CDates: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
CSpecies: A10186
RParChillil, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F.
ll., M.; Rutheford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
AltTitle: Genome sequence of Yerishia pestis, the causative agent of plague.
A.Reference number: AB0001; NCBI:U01704.13; PMID:11586360
AAccession: A10186
A>Status: Preliminary
AMolecule type: DNA
AResidues: 1-282 <KUR->
ACross-references: UNIPROT:Q8ZFZ0; GB:HL590842; PID:N:CAC90356.1; PID:g15979576; GSDB:GR
AGene: YPO15j3
CSuperfamily: inner membrane protein malK; ATP-binding cassette homolog

Query Match 11.9%; Score 79; DB 2; Length 282;
Best Local Similarity 22.0%; Pred. No. 3.6; Matches 45; Indels 14; Gaps 5;
Matches 27; Conservative 37; Mismatches

OY 13 KDGRDTLVLPNVPTNGVASIQAGAVPALREKRVTVSYOPSRRNKRYEVQKIQTNP 72
||::|:
Db 49 KNGARSVIIIGPRGCCGSTLLRLRS---LTFONGSIIRDQ-QDIQHAKYPARGQS 102
|||:
OY 73 ACTANGSCDPST-----ROKYADVFESFTQYSTDEBARFVRTLAALLASPLLDAID 126
||::|:
Db 103 LILSQASISSETIVFDLVRGRYAHSF-FHQMTSEDER-IYKAALAIAVNLESIVOQRVS 160
||:
OY 127 QLNL 129
||:
Db 161 ELIS 163

RESULT 12
TJ1660
Hypoetical protein COS41.6 - sea squirt (Cliona intestinalis)
CSpecies: Clona intestinalis
CDates: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
CAccession: TJ1660
R.Jbird, A.P.; Clark, V.; Jones, S.U.; Leighteb, S.; Dobson, R.; Tweedie, S.
submitted to the EMBL Data Library, December 1996

A;Map position: linear chromosome

Query Match	11.5%; Score 76.5; DB 2; Length 136;
Best Local Similarity	24.6%; Prod No 37;

Best Local Similarity 24.6%; Pred. No. 2.7;
Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

```

Oy 11 IGDROQTULVNPGRGNPNFNGVAASLQGAUV-----PALEKRTVYSVSGPSRRR 59
Db 3 ISDQKQTESADPNHMIEMWTGFTISTLLVAAAMGMIAYDIYRSPSEARREIANTVGEGQT 62
Oy 60 KNYKQVYQIQLTACIA-----NGSDPSVTRQKXADYTFESF-TQVSTBEARFYTE 111
Db 63 GQYRKAFALHNLSMTTAAQVAVNRKGDDEQGAAPENADVFIDYAASSKNGTLTFESD 120

```

Search completed: January 4, 2005, 09:17:32
Job time : 9.03224 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-10

Perfect score: 664
Sequence: 1 ARLEVTYLGNGKDGKQTLV.....AALLASPLLDALDQNLNAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181.seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.2	132	1	COAT_BPOBE
2	652	98.2	133	2	AAM33126
3	652	98.2	329	2	OBLTBL
4	652	98.2	329	2	AAL16663
5	563	84.8	133	2	Q9TOR9
6	563	84.8	329	2	O64307
7	543	81.8	133	2	Q9TOS0
8	543	81.8	329	2	O64303
9	528.5	79.6	132	1	COAT_BPSP
10	528.5	79.6	331	1	VAL_BPSP
11	496.5	74.8	132	2	Q9TOR8
12	496.5	74.8	330	2	O64310
13	116	17.5	131	1	COAT_BPPRR
14	96.5	14.5	473	2	Q8VDC2
15	89.5	13.5	530	1	TACY_LISSR
16	89.5	13.5	530	2	AAR97361
17	85.5	12.9	540	2	O48683
18	84.5	12.7	529	1	TACY_LISMP
19	84.5	12.7	529	1	TACY_LISMO
20	84.5	12.7	529	2	O9LSB9
21	84.5	12.7	529	2	O6E942
22	84.5	12.7	529	2	O6E942
23	84.5	12.7	529	2	O6E9G2
24	84.5	12.7	529	2	O6E9Q2
25	84.5	12.7	529	2	O6E9Q2
26	84.5	12.7	529	2	O6E9A28
27	84.5	12.7	529	2	O6E9A46
28	84.5	12.7	529	2	O6E9A47
29	84.5	12.7	529	2	O6E9A48
30	84.5	12.7	529	2	O6E9A49
31	84.5	12.7	529	2	AAT03000

32	82	12.3	1624	2	Q9V3K8	Q9V3K8 drosophila
33	82	12.3	1637	2	Q9SRU8	Q9SRU8 drosophila
34	81	12.2	336	2	O6TRF3	O6TRF3 mechanosarc
35	80.5	12.1	528	1	TACY_LISIV	P31831 listeria iv
36	80.5	12.1	528	2	O6R6D9	O6R6D9 listeria iv
37	80.5	12.1	528	2	AAR97343	AAR97343 listeria
38	80.5	12.1	1502	1	CYP1_YEAST	P12351 saccharomyc
39	79	11.9	282	2	O6ZFZ0	O6ZFZ0 yersinia pe
40	79	11.9	282	2	AAS61663	AAS61663 yersinia
41	79	11.9	432	2	P91584	P91584 citra intes
42	79	11.9	512	2	O6HGA7	O6HGA7 bacillus th
43	78.5	11.8	525	2	O6R6D0	O6R6D0 listeria iv
44	78.5	11.8	525	2	AAR97352	AAR97352 listeria
45	78.5	11.8	1954	1	ASP_DROME	Q9VC45 drosophila

ALIGNMENTS

RESULT 1
COAT_BPOBE STANDARD; PRT; 132 AA.
ID COAT_BPOBE
AC P03615; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alivolevirales.
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Dreilima D., Dislers A., Baumanns V.,
R Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RN Gene 137:133-137(1993).
[2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmona C., Sastre P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
RT bacteriophage Q-beta as an application of a mapping procedure for RNA
RT fragments.";
RN J. Biol. Chem. 253:8390-8399(1978).
[3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
RT and 60.";
RN J. Biol. Chem. 252:990-993(1977).
[4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiba T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RN J. Biol. Chem. 246:5003-5024(1971).
[5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Colohammi R., Fridborg K., Bundule M., Valgard K., Liljas L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RN Structure 4:543-554(1996).
-1- FUNCTION: Forms the phage shell; binds to the phage RNA.

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```
CC -----
CC DR EMBL; M99039; AAA16662.1; -
CC DR EMBL; V00643; CAA23992.1; -
CC DR PIR; A92240; VCBPOB.
CC DR PDB; LOBE; X-ray; A/B/C=1-132.
CC DR InterPro; IPR002703; Levi_coat.
CC DR Pfam; PF01819; Levi_coat; 1.
CC 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
CC KW INIT MET 0 0
CC FT CONFLICT 22 22 N -> D (in Ref. 4).
CC FT CONFLICT 56 56 Missing (in Ref. 4).
CC FT STRAND 6 9
CC FT TURN 13 14
CC FT STRAND 18 27
CC FT TURN 28 31
CC FT STRAND 32 36
CC FT HELIX 42 44
CC FT STRAND 47 53
CC FT STRAND 56 56
CC FT TURN 57 58
CC FT STRAND 59 59
CC FT STRAND 62 74
CC FT STRAND 83 96
CC FT TURN 98 99
CC FT HELIX 102 117
CC FT HELIX 119 126
CC FT TURN 127 127
CC SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;
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Query Match 98.2%; Score 652; DB 1; Length 132;
Best Local Similarity 97.7%; Pred. No. 3.4e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTTELAALLASPL 120
QY 121 LIDAIQDQNPAY 132
DB 121 LIDAIQDQNPAY 132
QY 121 LIDAIQDQNPAY 132
DB 121 LIDAIQDQNPAY 132
RESULT 2
AAM33126 PRELIMINARY; PRT; 133 AA.
ID AAM33126;
AC 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
OS Coat protein.
OC Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloleviratus; Alloleviratus subgroup IIT.
OC NCBI_TaxId=12009;
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes.";
RL BMC Evol. Biol. 3:24-24(2003).
DR EMBL; AY099114; AAM33126.1; -.
KW Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;
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Query Match 98.2%; Score 652; DB 2; Length 133;
Best Local Similarity 97.7%; Pred. No. 3.4e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRTVSVSOPSRRNK 60
DB 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRTVSVSOPSRRNK 61
QY 61 NKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTTELAALLASPL 120
DB 62 NKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTTELAALLASPL 121
QY 121 LIDAIQDQNPAY 132
DB 122 LIDAIQDQNPAY 133
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```
RESULT 3
OBLTEL
ID OBLTEL; PRELIMINARY; PRT; 329 AA.
AC OBLTEL;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloleviratus.
OC NCBI_TaxId=12009;
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes.";
RL BMC Evol. Biol. 3:24-24(2003).
[2]
RESULT 4
AAM33126 PRELIMINARY; PRT; 329 AA.
ID AAM33126;
AC 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
OS Coat protein.
OC Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloleviratus.
OC NCBI_TaxId=12009;
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozirovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; AY099114; AAM33127.1; -.
DR EMBL; M99039; AAA16663.1; -.
DR HSP; P03615; LOBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Levi_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;
```

Query Match 98.2%; Score 652; DB 2; Length 329;
Best Local Similarity 97.7%; Pred. No. 9.7e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRTVSVSOPSRRNK 60
DB 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRTVSVSOPSRRNK 61
QY 61 NKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTTELAALLASPL 120
DB 62 NKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVRTTELAALLASPL 121
QY 121 LIDAIQDQNPAY 132
DB 122 LIDAIQDQNPAY 133
```

Query Match 98.2%; Score 652; DB 2; Length 329;
Best Local Similarity 97.7%; Pred. No. 9.7e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DB A1 proteain.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievirub.
OX NCB1_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielesns I., Dreilima D., Dislers A., Baumanns V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; M99039; AAA16663.1; -
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.2%; Score 652; DB 2; Length 329;
Best Local Similarity 97.7%; Pred. No. 9,7e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTITGNTGKGRQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSOPSRNRK 60
DB 2 AKLEVTITGNTGKGRQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSOPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
AC Q9TOR9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievirub.
OX NCB1_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.
DR EMBL; AF059242; AAC14699.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR CoaT protein.
SQ SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;
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Query Match 84.8%; Score 563; DB 2; Length 133;
Best Local Similarity 82.6%; Pred. No. 1.4e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ARLEVTITGNTGKGRQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSOPSRNRK 60
DB 2 AKLEVTITGNTGKGRQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSOPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievirub.
OX NCB1_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.
DR EMBL; AF059242; AAC14700.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DDB52F15 CRC64;

Query Match 84.8%; Score 563; DB 2; Length 329;
Best Local Similarity 82.6%; Pred. No. 4.1e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ARLEVTITGNTGKGRQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSOPSRNRK 60
DB 2 AKLEVTITGNTGKGRQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVSOPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133
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RESULT 7
O9T0S0      PRELIMINARY; PRT; 133 AA.
ID O9T0S0;
AC O9T0S0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Coat protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9539761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR KM Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 098722B3C63A255 CRC64;

Query Match      81.8%; Score 543; DB 2; Length 133;
Best Local Similarity 79.5%; Pred. No. 1.2e-44;
Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

OY 1 ARLEVTITGNIGKDRQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTSVSQSSRRK 60
DB 2 AKLQAITISGIGKDDVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTSVSQSSRRK 61
OY 61 NYKVQVKIÖNPCTANGSCDPSVTRÖKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIÖNPCTANGSCDPSVTRÖKADVTFSFTQYSTDEERAFVTELAALLADPM 121
OY 121 LIDAIÖLNPAV 132
DB 122 LVNAIDNLNPAV 133

RESULT 8
O64303      PRELIMINARY; PRT; 329 AA.
ID O64303;
AC O64303;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Al-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=955239761; PubMed=7723040;

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RM RNP 1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35893 MW; 3E33CD821BE625F4 CRC64;

Query Match      81.8%; Score 543; DB 2; Length 329;
Best Local Similarity 79.5%; Pred. No. 3.5e-44;
Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

OY 1 ARLEVTITGNIGKDRQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTSVSQSSRRK 60
DB 2 AKLQAITISGIGKDDVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTSVSQSSRRK 61
OY 61 NYKVQVKIÖNPCTANGSCDPSVTRÖKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIÖNPCTANGSCDPSVTRÖKADVTFSFTQYSTDEERAFVTELAALLADPM 121
OY 121 LIDAIÖLNPAV 132
DB 122 LVNAIDNLNPAV 133

RESULT 9
COAT_BPSP      STANDARD; PRT; 132 AA.
ID COAT_BPSP;
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
RL -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
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DR EMBL; X07489; CA30374.1; -.
DR HSSP; P03615; IOBE.

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OC Allollevirus.
 RX NCBI_Taxid=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.U., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19 (1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.U., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSSP; P03615; 108E.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat_1.
 DR PROSITE; PS00030; RM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 961E5F408334410 CRC64;
 Query Match 74.8%; Score 496.5; DB 2; Length 330;
 Best Local Similarity 75.0%; Pred. No. 1.1e-39;
 Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
 QY 1 ALEVTYTGNIKDDRGQTLVLPNGVPTNGVASISQAGVPALEKRYTVSOPSRRNK 60
 DB 2 AGLNKVTLGLGKAGQVTLTPRGVPTNGVASISQAGVPALEKRYTVSVAQPSRRNK 61
 QY 61 NYKVQVQKIONPACTANGSCDPSVTQKADYVFSFYSTDERRAFVTELAALLASPL 120
 DB 62 NYKVQVQKIONPACTANGSCDPSVTQKADYVFSFYSTDERRAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADININPAY 132
 RESULT 13
 COAT_BPERR STANDARD; PRT; 131 AA.
 ID COAT_BPERR
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; leviviridae;
 OC unclassified Leviviridae.
 RX NCBI_Taxid=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhasee P., Vandeckerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1.";
 RL Eur. J. Biochem. 94:375-386 (1979).
 CC 1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 PIR; A04225; VCBP1.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat_1.
 KW Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7E639E1E50FC612 CRC64;
 OC

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0028;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTLVLPNGVPT-----NGVASISQAGVPALEKRYTVSOPSRRNKRYKVQV 66
 DB 4 QNLVLRKRAVATNDHTFPRDRIQVNGEVSTGVPIESRPTSLRKTSNGR--YKSTL 61
 QY 67 KIQNPT--ACTANGSCDPSVTQKADYVFSFYSTDERRAFVTELAALLASPLLI- 122
 DB 62 KLIVPVGSGTVANGVTVPVVATSVTVYDFVDASTTKERNINFGMTADAKDLMLVH 121
 QY 123 DAIDQINPAY 132
 DB 122 DTIVNLQGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2
 AC Q8VDC2;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Tmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kise H., Darai E., Kise C., Kost-Alimova M., Klein G., Dumanek J.P.,
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3.";
 RL Mamm. Genome 13:646-655 (2002).
 DR EMBL; AJ428064; CAD20986.1; -.
 DR MGD; MGI:2446841; Tmem7.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872B0E69F2A4D CRC64;
 Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.96;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;
 QY 5 TTTLGNIGKDGQTLV-----LNPGRVPTNG--VASISQAGVPALEK 46
 DB 195 TATCSNIISSQPSKVPQASKANPQASNPKNPKVSCSKPAPLPSLSKAREP 254
 QY 47 KTVTVSOPSRRNKRYKVQV-----KIQNPT-----ACTANGSCDPSVTQ- 87
 DB 255 KTVTVCSNIISSRSSSKVQMPQASRVNPQTSNPTNDRKISCTSPSTPRLLTIQQLSV 314
 QY 88 -----KVADYVFSFYSTDERRAFVTELAALLASPLLI 122
 DB 315 SPPAPAPCVIOMPSPTPIDGSRADVAKENTRSKTPK-----ALLSSPLLY 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligriolysin precursor (Thiol-activated cytolysin).
 GN Name=Igo;
 OC Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

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OX NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLCC;
RX MEDLINE=92182018; PubMed=1543752;
RA Haas A., Dumbeky M., Krefc J.;
RT "Listeriolysin genes: complete sequence of ilo from Listeria ivanovi
and of ilo from Listeria seeligeri.";
RL Blochin. Biophys. Acta 1130:81-84(1992).
CC -!- FUNCTION: Sulfhydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
Cholesterol is the receptor for the binding of these toxins to
eukaryotic cell membranes.
CC -!- SIMILARITY: Belongs to the thiol-activated cytolysin family.
CC -----
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CC EMBL; X60462; CAA42996.1; -
CC PIR; S22340; S22340.
DR HSSP; P19995; 1PFO.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACTTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
KW Cytolysis; Hemolysis; Lipid-binding; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 530
FT SITE 485 485 Binding to cholesterol (By similarity).
SQ SEQUENCE 530 AA; 59181 MW; 416F7A4D02029866 CRC64;

Query Match 13.5%; Score 89.5; DB 1; Length 530;
Best Local Similarity 25.0%; Pred. No. 5.2; Mismatches 37; Indels 43; Gaps 7;
Matches 34; Conservative 22;

OY 13 KDGRLTLV--NPRGVNPT-----NGVASLSQAGA-----VPALKRV 48
DB 94 KDGSEYIVVEKKKGKGINNNADISVINAISSLTYPGALVKANRELVENQPNVLPVKRDL 153
OY 49 TVSVSQPSNRKRYVQVKIQNPTACTANGSCDPSYTR--QKY-----ADVTFSPFQ 98
DB 154 TLSVDLPQMTKKDKNKIFVK--NPTKSNVNNAVNTLVERWMDKYSKAYPNINKIDYS--- 208
OY 99 YSTDERAFVRTTLAA 114
DB 209 ----DEMAVSESQLTIA 220

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